EXTENSION OF THE SHELF LIFE OF PLATELETS: PROSPECTS AND PITFALLS

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Under Faculty of Medicine

By

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2022

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I, Dr. Subhashis Das, hereby declare that thesis title: **EXTENSION OF THE SHELF LIFE OF PLATELETS: PROSPECTS AN PITFALLS** is original research work carried out by me for the award of Doctor of Philosophy in Medical Pathology.

Study is carried out under the supervision of Dr. Harendra Kumar. M.L, Professor, Department of Pathology, Sri Devaraj Urs Medical College, a Constituent Institute of Sri Devaraj Urs Academy of Higher Education and Research.

No part of this has formed the basis for the award of any degree or fellowship previously elsewhere.

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LIST OF ABBREVATIONS

AABB: Association of American Blood Banks

DGHS : Directorate General of Health Services

CDC: Centre for Disease Control

PLT: Platelet

MK: Megakaryocytes

TPO: Thrombopoietin

TAT: Turn-around time

ATP: Adeneosine Triphosphate

PAS: Platelet Additive Solution

MPV: Mean Platelet Volume

MPC: Mean Platelet Components

WB: Whole Blood

RBC: Red Blood Cell

WBC: White Blood Cell

EDTA: Ethylene Diamine Tetraacetate

FNHTR: Febrile non –hemolytic reaction

PCV: Polyvinylchloride

PCT: Plateletcrit

PDW: Platelet Distribution Width

FC: Flow Cytometry

VWF: Von Willebrand Factor

PAC: Monoclonal Anti-Platelet Antibody

PRT: Pathogen reduction technologies

PS: Phosphatidylserine

PFA: Platelet Function Analyser

GP: Glycoprotein

MP: Microparticles

PMP: Platelet Derived MicroPCs

TEG: Thromboelastography

MPC: Mean Platelet Component

ABG: Arterial blood gas analysis

MPM: Mean Platelet Mass

PMDW: Platelet Mass Distribution Width

P-LCR: Platelet Large Cell Ratio

IPF: Immature Platelet Fraction

pH: Potential of Hydrogen

TEHTM plasticizer: Tri-(Ethylhexyl)-Trimellitate

LDH: Lactate Dehydrogenase

AMP: Adenosine Monophosphate.

ADP: Adenosine Diphosphate

IMP: Inosine Monophosphate

TTBI: Transmission Transmitted Bacterial Infection

STR: Septic Transfusion Reaction

BGA: Blood Gas Analyzer

PGD: Pan Genera Detection

TAT: Turn Around Time

CMV: Cytomegalo virus

CFU: Colony forming units

MALDI-TOF MS: Matrix Assisted Lase Desorption Ionization Time-of-Flight Mass Spectrometry.

PSL: Platelet Storage Lesion.

TRALI: Transfusion-Related Acute Lung Injury.

ILs: Interleukins

TNF: Tumor Necrosis Factor

TCA: Tricarboxylic Acid Cycle.

FFA: Free Fatty Acid.

NADH: Nicotinamide adenine dinucleotide

NACO: National AIDS Control Organization

NBTC: National Blood Transfusion Council

NaCl: Sodium Choride

TCA: Tri Carboxylic Acid

MoAb: Monoclonal Antibody

ELISA: Enzyme Linked ImmunoSorbent Assay

CD: Cluster of Differentiation

FITC: Fluorescein Isothiocyanate

RANTES: Regulated on Activation, Normal T cell Expressed and Secreted

TTI: Transfusion transmitted infections.

CPD: Citrate Phosphate Dextrose

SAGM: Saline Adenine Glucose Mannitol

FFP: Fresh Frozen Plasma

BC: Buffy coat

PC: Platelet Concentrate

PTM: Post Transnational modification

DTT: Dithiothreitol

IAA: Iodoacetamide

HCD: High energy Collision Induced Dissociation

AGC: Automatic Gain Control

FDR: False Discovery Rate

MGF: Mascot generic files

GDP: Guanosine diphosphate

GTP: Guanosine triphosphate

iTRAQ: Isobaric tags for Relative and Absolute Quantitation

ICAT: Isotope Coded Affinity Tag

DIGE: Differential in Gel Electrophoresis

2D: Two Dimensional Gel Electrophoresis

PTM: Post Translational Modifications

BA: Blood Agar

CA: Chocolate Agar

MA: MacConkey Agar

SDA: Sabouraud Dextrose Agar

CPDA: Citrate-phosphate-dextrose solution with adenine

NSAIDS: Non-steroidal anti-inflammatory drugs

TA-GVHD: Transfusion-associated graft-versus-host disease

NA: Nucleic Acid Testing

POCT: Point of Care Testing

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INTRODUCTION

Platelet concentrates (PCs) are surprisingly multifunctional and are involved in many pathophysiological processes including hemostasis, thrombosis, clot retraction, vessel constriction and repair, inflammation including promotion of atherosclerosis, host defense and even tumor growth/ metastasis.[1]

There is increased demand for stored PCs for therapeutic transfusions such as treatment of patients with disorders resulting in thrombocytopenia and for patients who become thrombocytopenic after chemotherapy or any major surgeries invasive procedures, such as cardiac surgery. High platelet quality would be expected to result in improved clinical efficacy, determined by count increment, improved hemostasis and lower risk for adverse reactions in recipients.[1]

Reduction of functional aspects of PCs while undergoing preparation and storage is referred as "platelet storage lesion" (PSL)[2] secondary to platelet activation. This is characterized by decreased hemostatic efficacy post transfusion along with poor post-transfusion recovery. Activation of PC is associated with changes in platelet morphology, biochemistry, granule release, and surface glycoprotein expression. Hence, the quality of PC is an important issue in transfusion therapy.[2]

Transfusion of PCs is of great clinical significance and is associated with similar risks as that of blood transfusion viz for example the risk of transmission of infectious diseases and allo-immunization. During the process of hemostasis, PCs become activated and stop the bleeding. This function may be greatly compromised by the onset of PSL which affects the PCs both structurally and functionally, along with their metabolic activities. Mainly improper blood collection, storage and preparation contribute to these lesions. During storage the oxidation of long-term fatty acids is impaired, leading to an increase in glucose consumption, decrease in potential of Hydrogen (pH) and lactate production, all leading to eventual PSL.[2]

Broadly PCs are produced by two methods- namely 1) whole blood (WB) derived PCs: a) platelet rich plasma (PRP) b) Buffy coat derived platelet (BC-PC) 2). Single donor PCs (Apheresis).[3]

Due to increased use and development of cancer therapy demand for PC transfusion has gone up steadily over the years. Limited availability of PCs is because of limited shelf-life of 5 days. This is due to a) development of PSL and b) potential microbial contamination during storage period. Hence every year several units of PC are being discarded.[3]

Multiple approaches are being explored in order to maintain a comfortable stock position and to minimize the wastage. To maintain a comfortable stock position regular donor recruitment drive should be conducted with proper platelet inventory management. Donor recruitment drives, along with stringent donors selection process is a labor intensive and logistically complicated procedure which makes it a costly exercise. Hence, our effort is examine the possibility of PCs shelf-life extension beyond 5 days by proper scientific management leading to better platelet utilization with consequent wastage reduction of this precious resource.[3]

Quality parameters	Quality Research	monitoring
pH Platelet yield, PC volume	MPV, pH, Glucose,Lactate PO_2 PCO_2 Platelet activation (P-selectin) Morphology (Score)	Annexin –V (apoptosis) Platelet aggregation Platelet Protein Analysis Platelet additive solution

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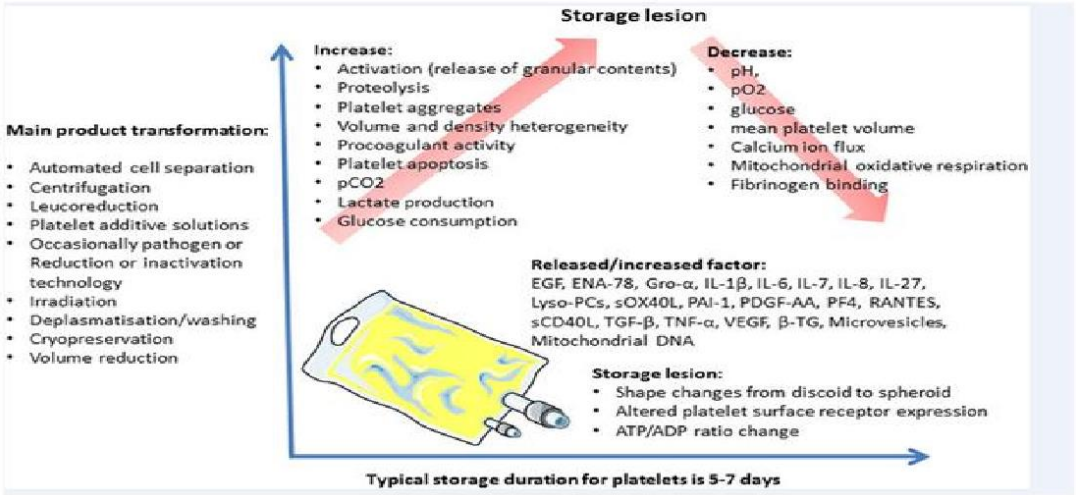


Figure 1: Factors affecting platelet storage lesion (adopted from Fritsma GA2015;28(2):125-31)[1]

REVIEW OF LITERATURE

PCs were first described by Giulio Bizzozero during 1881-1882.[4] Estimation of PC count in patients was first noted by Duke in 1910.[4] Dr. Scott Murphy and Frank Gardner provided evidence that PCs could be stored at 22 ± 2^0C till 3 days.[5] Megakaryocytes were first identified by Wright as the precursor cell to the PCs whereas Skripchenko et al. concluded that prolonged periods of increased carbon dioxide(CO_2) levels are accompanied by poor pH control and platelet mitochondrial dysfunction during storage.[6]

Around 20% of PCs undergo wastage due to numerous reasons which may show seasonal and geographical variations.[7] For example European data, show discard of PCs due to expiry range from 1-20% whereas out dating of PCs has been noted as 21% in Australia.[8]

Further, complicating the issues is the huge clinical demand for PC transfusion as over the last decade there has been 15-16% rise in requirement for PCs. Possible causes for this rising demand include an increasing and aging population, increased prevalence of hematological malignancies, and changes in management of hematological malignancies, resulting in requirement for greater PCs support.[9]

The extension shelf life of PCs will help better the platelet inventory logistics by ensuring uninterrupted supply for extended period while also help in reducing the wastage. Numerous studies in the field of Operations Research have attempted to predict the impact on wastage by extending the shelf life. Haijema et al set a dual strategy consisting of stochastic dynamic programming along with simulation model to develop an ordering strategy to decrease wastage and shortages.[10] Identical findings were noted by Kort et al with regard to a platelet inventory management in a Dutch blood bank.[7]

Platelets are small, a nucleate, measuring 1 to 6μm in diameter, derived from megakaryocytic (MK), cytoplasm, playing an vital role in hemostasis, inflammation and immunity. PCs production is regulated by thrombopoietin (TPO). MK produces platelets by cytoplasmic shedding directly into bone marrow sinusoids. About 1000-5000 platelets are produced by each MK before undergoing apoptosis. In normal individuals platelets production is approximately 35,000-50,000 uL of whole blood/day. Exogenous TPO administration can increase PCs production rate to 20-fold.[11]

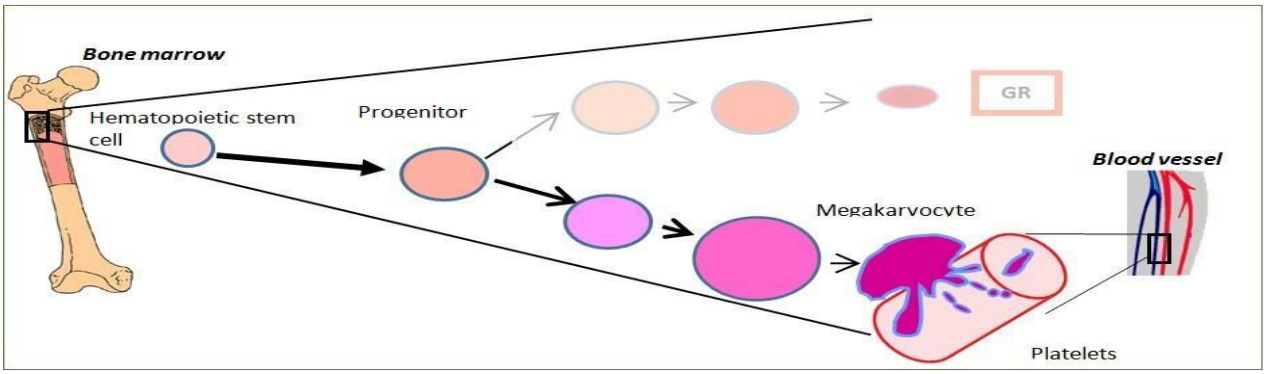


Figure 2: Various stages of platelet formation. (adapted from Paulus JM 1975; 46 (3): 321–36)[12]

MK increase in size during maturation and expand their cytoplasmic content to develop cytoplasmic processes called progenitor platelets, which results in the release of thousands of platelets. The circulating lifespan of platelets is approximately five to nine days in mammals and as they age, platelets are removed from circulation by macrophages in the liver and spleen.[2]

Platelet Structure: (Figure-2)

Platelet membrane surface is called the glycocalyx and it serves to transport albumin and fibrinogen to storage organelles by endocytosis. Important protein membrane receptors are glycoprotein complex IIb-IIIa (GPIIb-IIIa) and glycoprotein complex Ib-IX-V (GPIb-IX-V). The (GPIb-IX-V) complex is known as the von Willebrand factor (VWF) receptor and serves as an initiator of platelet adhesion at high-shear rates and the membrane complex GPIIb-IIIa is the fibrinogen binding site receptor and mediates platelet aggregation to ensure thrombus formation.[2]

PCs integrity and shape are maintained by the cytoskeleton which consist of the microtubules, actin, ankyrin, calmodulin, calpain, dystrophin, spectrin, protein 4.1, talin, vinculin, fibrinogen and vWF receptors and glycoproteins. Microtubules are arranged in a coil, forming a platelet marginal band mainly located in the cytoplasm. It is also required for the formation and release of PCs by MK.[2]

Platelets contain three different types of secretory granules: alpha granules, dense granules and lysosomes. The alpha granules are the largest and most abundant and they have several adhesion proteins that play a vital role in hemostasis, as well as glycoproteins involved in

wound healing and inflammation.[2] The dense granules are the smallest granules which have many pro-aggregation factors like calcium, ATP, Adenosine Diphosphate (ADP), serotonin and pyrophosphate. Platelet lysosomes contain digestive enzymes (hydrolases) able to degrade glycoproteins, glycolipids and glycosaminoglycans important for eliminating circulating platelet aggregates. The mitochondria along with the dense tubular system constitute the smooth endoplasmic reticulum membrane system. The mitochondria fulfills the energy requirements for platelet secretion and aggregation. Synthesis of platelet prostaglandin and thromboxane takes place in the dense tubular system, where calcium stores are also present.[2]

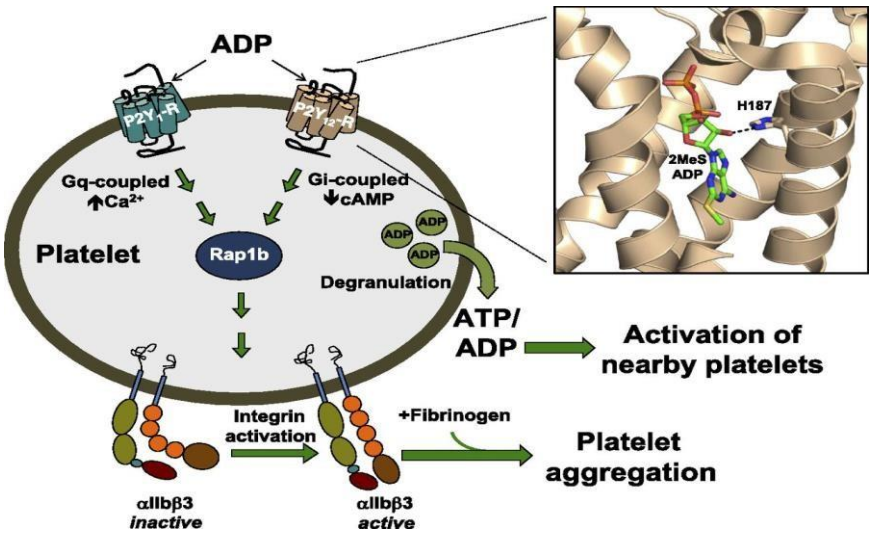


Figure 3: Showing features of PCs metabolism. (adapted from Brodsky RA. 2014;124(18):2804-11).[13]

Alpha granule membrane proteins: (Figure-3)

P-selectin (also known as granule membrane protein 140 or CD62P) is the most well-known alpha granule membrane glycoprotein expressed on the surface of activated PCs.[1] there exist an inverse relation between in-vivo platelet recovery and in-vitro P-selectin expression, therefore, P-selectin expression may serve as a useful PC quality control parameter.[1]

The glycoprotein complex IIb/IIIa (also known as GPIIb-IIIa, CD41/CD61 and Integrin αIIbβ3a) is the most common receptor of the platelet membrane and functions as a fibrinogen binding site. GPIIb-IIIa is always present in the activated PCs, non-activated PCs and membrane of the alpha and dense granules.[2]

When platelets are activated, the platelet surface GPIIb-IIIa complex undergoes conformational changes that result in expression of epitopes detectable using murine

monoclonal anti-platelet antibody (PAC- 1) by flow cytometry (FC). The PAC-1 antibody binds only to activated PCs; therefore, its quantification is an important marker of PC activation. Presence of activation markers (P-selectin) and increase in GPIIb-IIIa surface expression has been found to have a dependent relationship in platelet concentrates.[2]

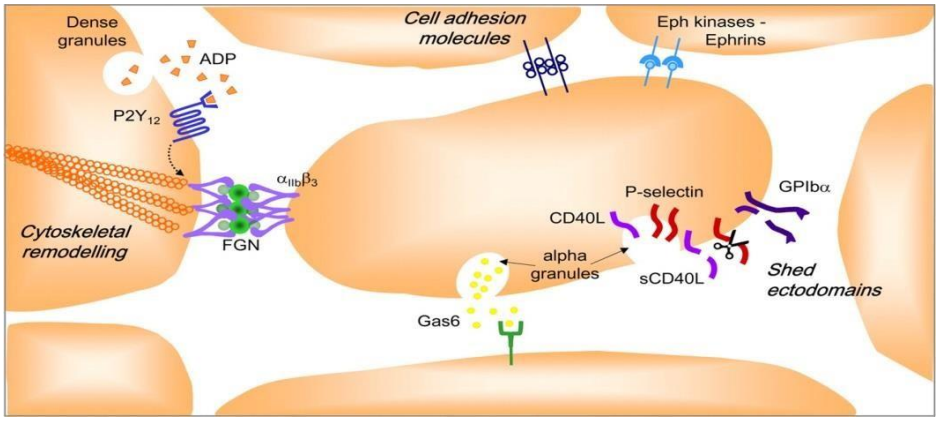


Figure-4

Figure 4: Mechanism of release of platelet alpha granules. (adapted from Hampton T, 2018;319 (13): 1311–12).[14]

Apoptosis markers: (Figure-5)

Apoptosis is characterized by morphological and biochemical changes including cellular shrinkage, membrane blebbing, karyorrhexis and fragmentation. There are many techniques to identify and quantitate apoptosis, but FC is the gold standard method[1]

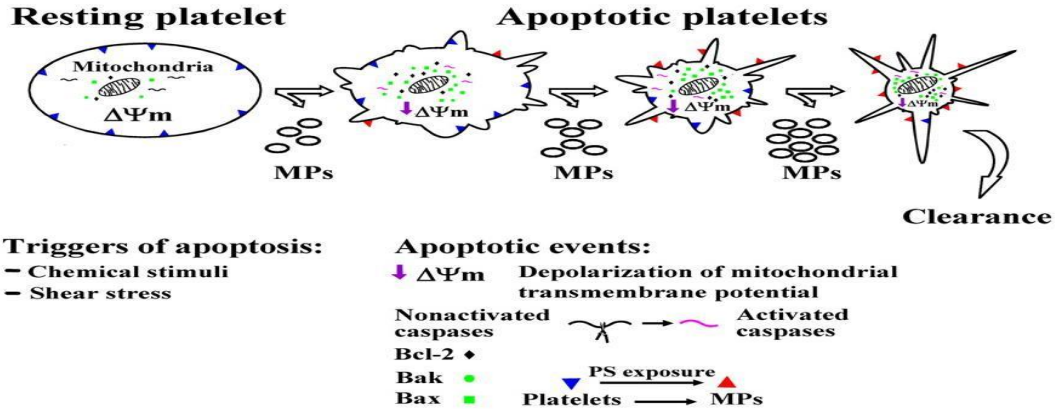


Figure-5

Figure 5: Showing mechanism of apoptotic of platelet. (adapted from Fritsma GA2015;28(2):125-31).[1]

Phosphatidylserine: (Figure-6)

Translocation of a phospholipid called phosphatidylserine (PS) it is important cellular alteration during apoptosis .The cytosolic side of the cellular membrane to the outer layer, by which PS becomes exposed on the external surface of the cell membrane. Annexin V is a calcium-dependent protein with a high affinity for PS is used as a sensitive indicator of PS exposure on the cell membrane surface making it a valuable tool to detect early apoptosis.[2] Increased PS expression on platelet surface has been reported in human stored PCs after 3 to 5 days. This shows a positive correlation between increased expression of PS on the cell membrane, and increases in platelet storage lesions and decreased platelet viability, therefore it is considered to be a valuable tool for assessing the quality of PC.[2]

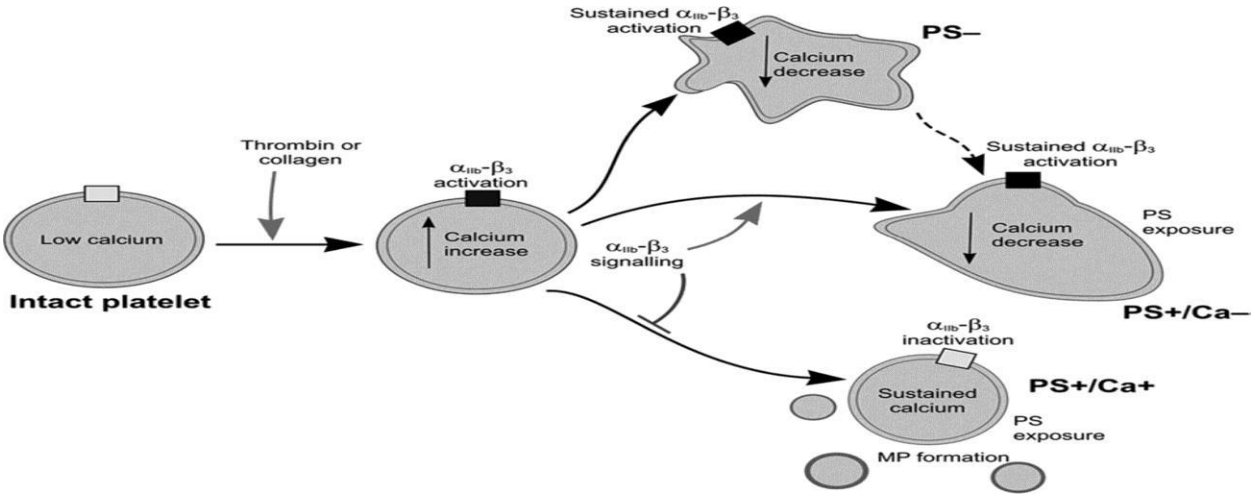


Figure 6: Showing mechanism of release of Phosphatidylserine of platelet. (adapted from Fritsma GA2015;28(2):125-31).[1]

Caspase 3**:** (Figure-7)

In PC it has been proven that caspase 3 activation is a late event during platelet storage and increases during storage time, while decoy receptor 2 expressions (a tumor necrosis factor [DcR2]) on the plasma membrane is an early event during platelet storage, therefore, quality of stored PCs may not be improved by caspase inhibitors.[2]

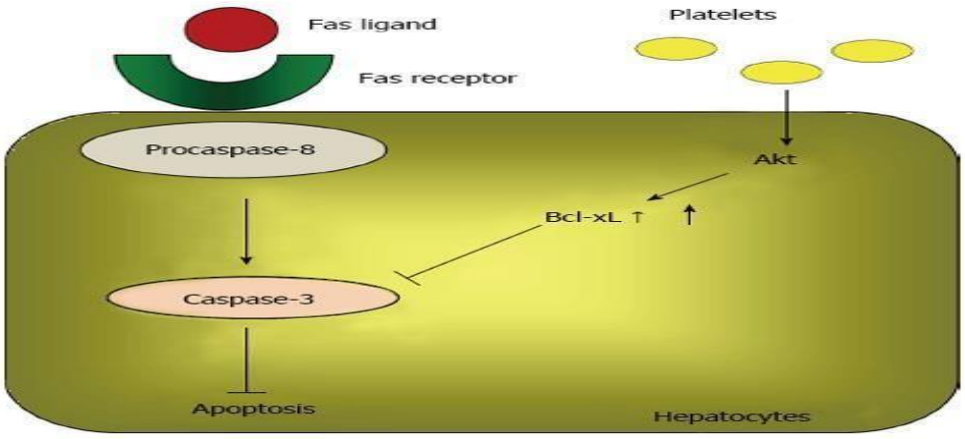


Figure-7

Figure 7: Mechanism of release of platelet apoptosis. (adapted from Fritsma GA2015;28(2):125-31).[1]

Platelet Metabolic activity: (Figure 8)

In an attempt to improve PC quality and increase its shelf life, some researchers have tried to add glucose to the media. An increase in glycolysis is seen on excessive glucose consumption, which causes an increased production of lactic acid, acidifying the PCs media. A decrease in pH below 6.2 or an increase above 7.3 in stored PCs can cause irreversible platelet damage and has been associated with substantial loss of platelet viability.[2]

Ratio of media concentrate to PCs ratio can affect the pH. In highly concentrated platelet products there will be more nutrient consumption and platelet activation; this will be reflected as a shorter shelf life.[2]

Main energy source for PCs is ATP. Different metabolic pathways using different substrates can generate ATP and produce different final products.[2] The tricarboxylic acid (TCA) cycle is an oxygen-dependent pathway that provides approximately 85% of ATP to the platelet using free fatty acid substrate and producing CO_2 in plasma. Glycolysis is an anaerobic pathway that provides approximately 15% of ATP using glucose as a substrate and producing lactate. Oxygen level in the platelet storage container has a significant impact on platelet quality, so both pO_2 and pCO_2 have been assessed to determine appropriate gas exchange during storage.[2]

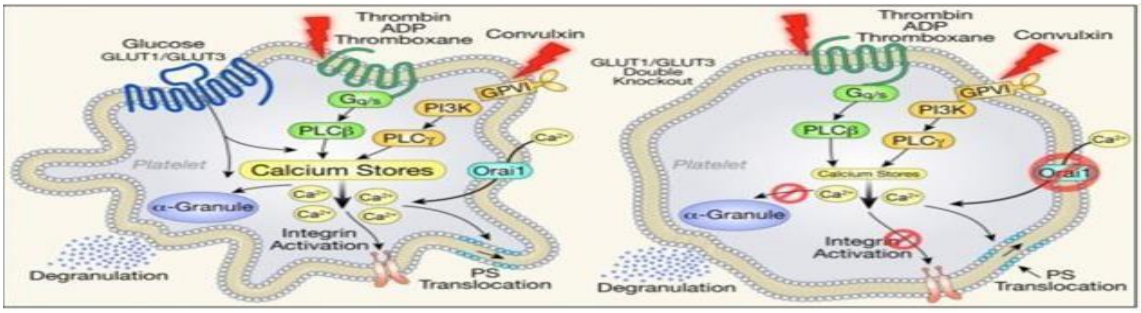


Figure 8: Glucose metabolism and platelet activation (adapted from Fritsma GA2015;28(2):125-31).[1]

Platelet activation is reflected by multiple cellular changes and can be induced by diverse upstream inputs. Platelet activation requires glucose uptake that leads to the mobilization of intracellular calcium stores. Preventing platelet glucose uptake impairs platelet calcium metabolism that reduces activation of PCs along with platelet death and clearance from the circulation.[1]

Platelet micro particles (PMPs): (Figure 9)

The presence of micro particles in platelet-rich plasma has first been described in the late 60s, where these were called as platelet dust. Platelet micro particles (PMPs) are released from PCs upon activation or apoptosis. PCs contain PMPs in the supernatant, reflecting activation during collection, and/or storage.[15]

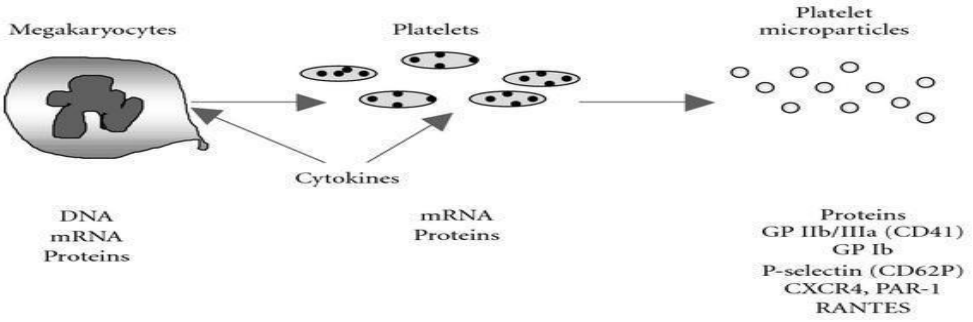


Figure 9: PMPs are phospholipid microvesicles of 0.1–1 micron in size, sheded from parental cell fragments after stimulation with physiological agonists such as thrombin or collagen or exposure to shear stress (i.e., in severe stenosis). PMPs express functional adhesion receptors, including GPIIb/IIIa (adapted from Vassallo RR, 2006;13(5):323-30).[3]

Platelet Activation: (Figure 10)

Platelet activation is required for formation of the definitive platelet plug. Different molecules released under certain conditions such as with endothelial damage, inflammation, neoplasia, or immune-mediated processes can trigger activation. During activation, the platelet undergoes a series of events that begins with an agonist-receptor interaction which leads to shape change, granule content release, increase in volume and an increased expression of protein receptors on the cellular membrane.[11]

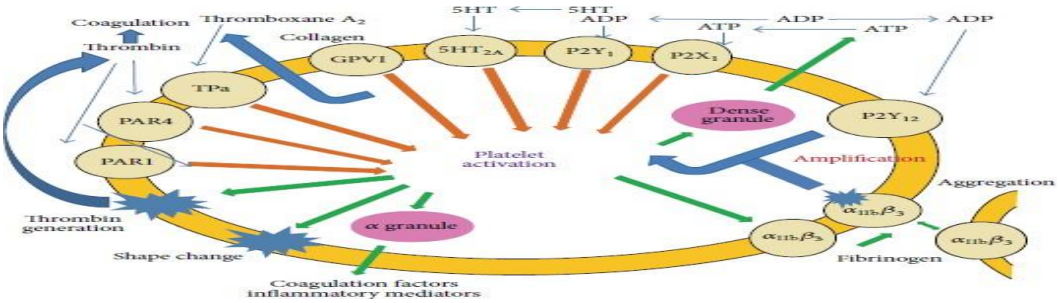


Figure 10: Platelet-activation mechanisms and role of the P2Y12 receptor. Platelet activation leads to dense-granule secretion of ADP, which activates P2Y12, inducing amplification of aggregation, procoagulant, and proinflammatory responses (adapted from Storey, 2008;10:30-7).[16]

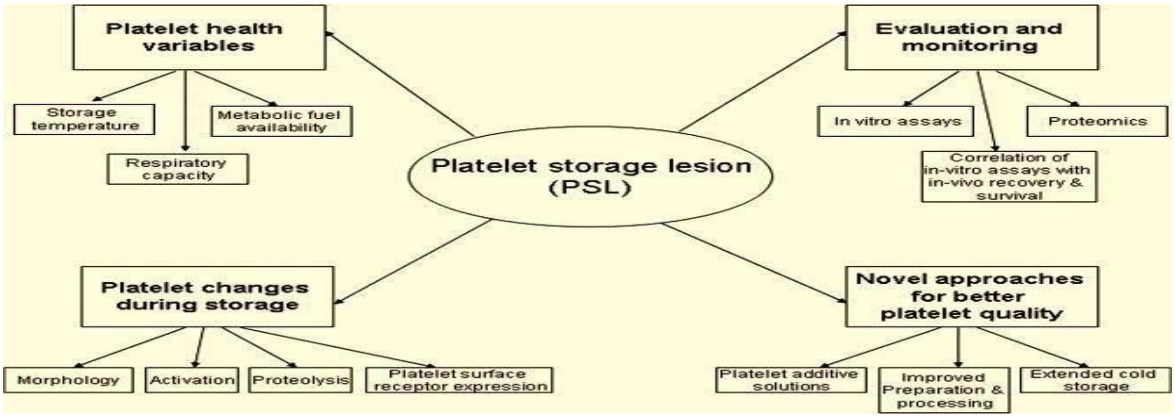


Figure 11: Various mechanism of Platelet storage lesion (PSL) (adapted from Guppy M et al 1990;59:146-152).[11]

Table-1: Factors influencing the development of PSL.[11]

1	Collection techniques	• Composition of anticoagulant • Preservative solution • Blood flow rate • Ratio of anticoagulant • Centrifugation force resting period before re-suspension
2	Storage conditions	• Temperature and storage period • Cellular content • Volume and composition of suspension media • Final plasma concentration in storage media • Type of agitation • Pack size
3	Storage containers	• Plastic bag composition • pH Estimation • Thickness of plastic • Gas transfer properties of plastic • Thickness of container wall
4	Treatment after collection	• Extent of leuko depletion, • Extent of plasma removal UV-B irradiation y-irradiation • Cryopreservation, • Lyophilisation

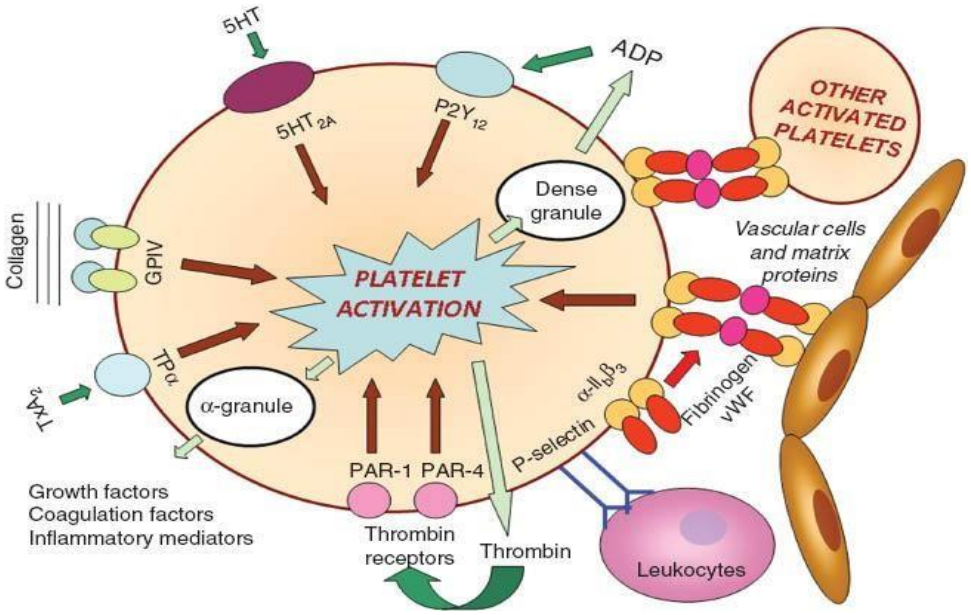


Figure 12: Pathways of platelet activation. (adapted from Farre AL et al. 2014 ;18(1):27-36).[17]

1. Factors affecting Platelet storage lesions

A. Temperature and bacterial contamination

The environmental factors that can have impact on stored PC is temperature. It has been demonstrated that colder temperature delays bacterial growth but causes detrimental changes to the platelet membrane leading to morphological changes and platelet activation along with reduction of platelet recovery, function and survival.[18] Therefore, the optimal temperature to store PC is suggested to be between 20^0C to 22^0C.[18]

B. **Agitation method**

Continuous gentle agitation during storage is essential for adequate diffusion of gases through the gas-permeable plastic containers.[19] In some studies, it was proven that non-elliptical continuous agitation of the PC improves the oxygenation of the cells and delays activation onset. In another study, elliptical, circular and flat-bed agitators were compared; a significant decrease of pH was observed in PC stored on the flat-bed agitator after the fourth day, platelet activation was higher in the units stored on the elliptical rotator, and the flat-bed shaker could not re-suspend the platelet pellet after centrifugation, therefore, circular rotation was determined to be the preferred method.[19]

C. **Storage containers**

Appropriate storage containers must maintain sufficient oxygen (O_2) and carbon dioxide (CO_2) permeability. First and second generation polyvinylchloride (PVC) storage containers were limited to 3 and 5 day storage respectively, due to the decline in pH to less than 6.0 which was associated with loss in PCs survival (which correlated with low platelet morphology scores). Third generation PVC storage containers plasticized with butyryl-tri-n- hexyl-citrate have shown better permeability resulting in good in vivo PC characteristics following transfusion.[20]

D. **Storage Media**

Platelet storage media is the fluid in which the PCs are suspended and it is important for providing different nutrients to the stored PCs, and for maintaining metabolic functions; the lack of these nutrients accelerates platelet activation and promotes apoptosis. Platelet Additive Solution (PASs) are synthetic solutions containing several nutrients in addition of 30% of plasma. Studies have shown numerous benefits of PAS over plasma particularly with regard to increased post transfusion survival of PCs and decreased post transfusion reactions.[21]

Gulliksson highlighted some other characteristics in using an additive solution for substitution of plasma as a storage medium for PCs.[22] In brief these are: (a) An extended shelf-life while still retaining the hemostatic properties of PCs (b) The presence of glucose in the platelet storage medium, necessary to retain metabolic activity of the PCs, avoids platelet lesions(c) Acetate used as an additional substrate for platelet metabolism, help in reducing lactate production , which in turn maintains a stable pH during storage.[22]

Table 2: Comparative study of various composition of platelet additive solution. (adapted from Adams GA. 1987; 52(4):305-12).[23]

Composition	TSol (PASII)	Composol (GAC)	InterSol (PASIII)	SSP + (PASIIIM)	GASP-BIC
NaCl	115.5	90.0	77.3	69	110
Acetate	30	27	28.2	41	15
KCl	-	5	-	5	5
$MgCl_2$	-	3	-	1.5	3
$Na2HPO^4$	-	-	28.2	26	4
Na^3-citrate	10	10	10.8	10	-
Citric acid	-	-	-	-	7.5
Gluconate	-	30	-	-	-
Glucose	-	-	-	-	30
pH	7.2	7	7.2	7.2	5.2

Leukoreduction:

Leukoreduction is the removal of leukocytes from the blood or blood components to produce a Leukoreduced product. Leukocytes plays a vital role in post-transfusion febrile non-hemolytic reaction (FNHTR).[24] The presence of leukocytes causes increased consumption of glucose and decreases the energy substrate in the media, leading to the onset of PSL. Hence, in some countries leukoreduction is performed as a mandatory step in PC preparation using leukofilters.[21]

LACUNAE OF KNOWLEDGE

Although efforts have being made to improve platelet transfusion services and ensure of optimum management of platelet inventory serious challenges remains to be resolved because of the following reasons 1) The limited shelf life of PCs remains a serious handicap towards maintenance of adequate platelet inventory poses significant challenges to platelet inventory management, especially in small hospitals located in remote regions where it is difficult to maintain sufficient platelet inventories to support transfusion services particularly at times of increased demand; 2) Progressive increase in clinical demand for PC transfusion on a global scale 3) Limited universal access towards latest platelet screening technologies to ensure platelet safety and viability 4) Potential storage related hazards along with adverse implication because of accumulation of bio-reactive substances.[25]

Before finally deciding to extend the shelf life of PCs it is of paramount importance to carefully assess the risk, safety and benefits of the product with the extended duration as any deleterious effect will have serious consequences to the recipients with adverse clinical outcome. However, reduction of platelet storage time may result in unnecessary wastage leading to severe shortages particularly, during the time of crisis. Few studies have already being done in this regard but more studies are warranted to have a better and comprehensive understanding regarding the various clinical requirements, efficacies and safety of PCs without compromising quality parameters during extended storage in order to define the best practice of optimizing platelet inventory management while emphasizing platelet transfusion safety.

Hence, more research and development efforts towards extending the shelf life of PCs are required to ensure that safe platelet product having all the necessary quality parameters are readily available particularly in rural and resource constraint set up where access to healthcare is very limited.

Figure 13: Risk benefit aspects regarding platelet safety versus platelet quality (adopted from Estcout LJ et al. 2014;24(5):260-68)[9]

AIM OF THE STUDY

The principal aim of the study is to establish whether there is scope for further initiatives for validation of the introduction of new procedures leading to the review of current policy regulating the storage shelf-life of PCs, which is not allowed to exceed 5 days.

The objectives are as follows:

1. To undertake comparative evaluation of various PCs preparation techniques with regard to extended storage period.
2. Determination in vitro quality of stored PCs of seven-day duration.
3. Mapping way forward for further initiative.

MATERIALS AND METHODS

The study was performed in the blood Centre of R.L Jalappa Hospital and Research Centre, attached to the Department of Pathology, Sri Devaraj Urs Medical College (SDUMC), a constituent of Sri Devaraj Urs Academy of Higher Education and Research (SDUAHER), Kolar, Karnataka. Donor selection was performed using standard operating procedures (SOPs) based on the national guidelines[2] and which was undertaken under the supervision of qualified medical officer following the submission of informed written consent of the donor to participate in the study. Prior approval from the institutional ethical committee (IEC) was also obtained.

The following preparation methods of PCs were undertaken in our study; which includes the following,

1. **PRP-PC preparation method:**

WB is centrifuged by soft spin to prepare PRP followed by a high speed centrifugation to obtain a platelet pellet. Most of the plasma is removed, and the platelets are stored in a reduced volume of remaining plasma or in a synthetic medium.[2] (refer Figure-12)

2. **BC-PC preparation method:**

WB is centrifuged at high-speed to prepare a BC. The BCs are pooled (of ten with a storage medium) and centrifuged to a platelet rich supernatant that is transferred to the storage container. Which are made of PVC plasticised with butyryl-tri-n-hexyl-citrate having good gaseous permeability and resulting in satisfactory in vivo viability of PCs following transfusions.[2] (refer to Figure-14)

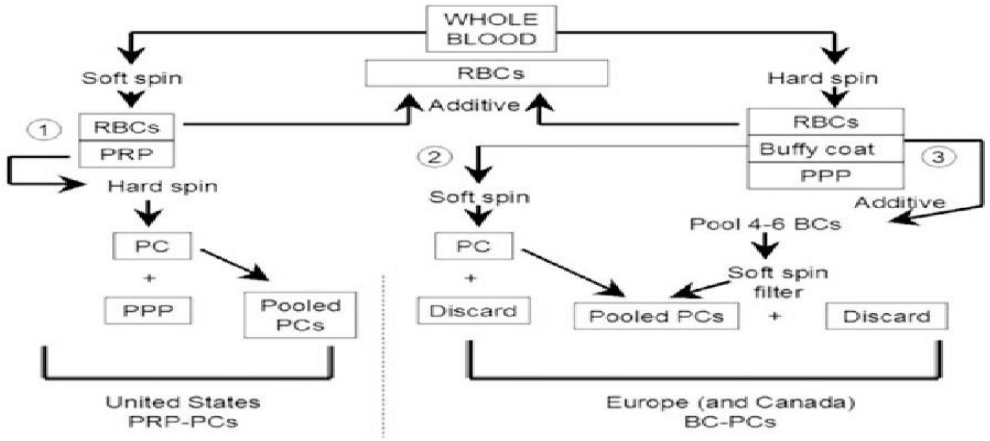


Figure 14: comparative study of procedure from PRP –PC and BC-PC. (adapted from Ringwald J.2006).[21]

Each of the PCs unit prepared by different methods will be assessed based on the following parameters:

i. Platelet concentrate (PC) volume
ii. Swirling
iii. Platelet count/bag
iv. WBC count/bag
v. pH changes

In this study we will analyze the quality of different platelet concentrates prepared by different methods as per the recommended DGHS (Directorate General of Health Services) quality norms. [Table 3].[26]

Table 3: Standards for platelet concentrates as required by the AABB (Association of American Blood Banks) and DGHS technical manual, 2nd ed.)[26]

Quality Parameters	PRP-PC	BC-PC	Apheresis-PC
Volume	40-70ml	70-90ml	200-300ml
Swirling	Present	Present	Present
Platelet count/bag	$>5.5 \times 10^{10}$ in 75% of unit tested	$>5.5 \times 10^{10}$ in 75% of units tested	$>3 \times 10^{11}$ in 75% of units tested
WBC count/bag	$5.5 \times 10^{7} - 5 \times 10^{8}$	$5.5 \times 10^{7} - 5 \times 10^{8}$	$< 5 \times 10^{6}$
pH	>6.0 at the end of maximum days of storage in 100% of units tested	>6.0 at the end of maximum days of storage in 100% of units tested	>6.0 at the end of maximum days of storage in 100% of units tested.

Methods:

1. Platelet concentrate volume: Estimation of platelet volume represents the presence of plasma which in turn, acts as a buffering agent and is responsible for pH regulation.
The PC volume is calculated by the following formula,

$$\text{Volume of PC} = \frac{\text{Weight of full bag} - \text{Weight of empty bag}}{\text{Specific gravity}}$$

The specific gravity includes (1.053 for whole blood, 1.03 for PRP-PC and 1.06 for BC-PC, respectively).

2. **Swirling:** Evaluation of swirling is a simple noninvasive method that can be performed by visual inspection and is useful for routine quality control.[26] Visual inspection of swirling correlates with platelet morphology.

Table 4: Scoring of Swirling

Score 0	Homogenous turbid and is not changed with pressure.
Score 1	Homogenous swirling only in some part of the bag and is not clear
Score 2	Clear homogenous swirling
Score 3	Very clear homogenous swirling throughout the bag

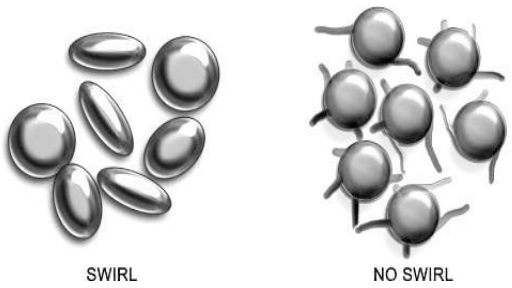


Figure 15: Scoring of Swirling
(Adopted from Mathai, J., Resmi, K. R., Sulochana, P. V. (2006). Platelets 17(6). p.393–396)[27]

1. **Platelet count per bag:** Usually the PRP samples have a lesser volume as compare to BC-PC because of the PRP preparation methodology results in 21% of plasma and 19% of the platelets getting restricted to the infranatant RBCs. The platelet count per bag is done by multiplying platelet count/µl with product volume using a routinely calibrated automated hematology analyzer, (Sysmex XE 2100 analyzer Sysmex Corporation, Japan).[28]

2. **WBC count per bag:** Presence of WBC is associated with deleterious clinical affects and is responsible for Febrile Non Haemolytic Transfusion Reactions (FNHTR) and Graft Versus Host Disease (GVHD) in transfused individuals.[29] The WBC count per bag was performed multiplying WBC count/µl with whole blood volume using a routinely calibrated automated haematology analyser, (Sysmex XE 2100 analyser Sysmex Corporation, Japan).

3. **pH changes:** The principle of the operation is measurement of the potential of a specific ion in solution against a stable reference electrode of constant potential. The method is based on the technique of potentiometry, which is the measurement of electrical potential without a current flowing. pH of all samples was measured immediately after sampling at a temperature of 22^0C using handheld pH meter [Eutech pH Tutor].[26] The electrode of pH meter was placed in PCs and swirled the solution. The pH reading had to be stabilized before the pH result of PCs taken. When the reading was freezed, the pH of PCs was recorded.

4. **Platelet function test:**[27] It is used for platelet aggregometry for detecting inherited and acquired platelet defects along with monitoring of anti-platelet drugs.

Table 5: Major platelet function tests and their clinical applications[27]

Test	Clinical use
Platelet aggregometer	Wide spread uses ranging from basic and clinical research to in vitro assessment of the aggregatory effects of agonists (platelet activation factor (PAF), thrombin, collagen etc along with the anti-aggregatory effects of bioactive antiplatelet compounds.
PAF	PAF is produced in limited quantities by platelets, endothelial cells and macrophages etc which causes platelet aggregation of blood vessels along with inflammatory response.

5. Sterility: BacT/ALERT 3D (BioMerieux, USA)is a FDA approved, automated colorimetric blood culture method based on CO_2 detection was is used for assessing bacterial contamination of PCs. Depending on the amount of CO_2 any microbial growth was detected by color sensor located at the bottom of the bottle. released color of the pH sensitive liquid sensor which is located at the bottom of the bottle changes.[28]

6. Platelet additive solution (PAS): PAS is a platelet storage medium which develops to limit the serious side effects of plasma and promote extension of the shelf life of the product and help maintain the quality parameters of the PC.[30]

7. Flow cytometry (FC): FC has emerged as a powerful tool for the study platelet function. Platelet activation is associated with surface expression of proteins not found on quiescent PCs. Analysis of such proteins is used for evaluation of PC activation.[31]

8. Proteomics: It involves analysis of the full complement of proteins at a given time. The basic principles include: a) Preparation of a complex protein mixture. b) Separation of protein mixture. c) Characterization of proteins within mixture.[32]

Study Samples: Samples of PCs prepared from the blood bags of voluntary blood donors.

Sampling Technique: Simple random sampling method.

Sample size of our study calculated based on the study done by Varshashree et al[33]on the basis of the following formula,

Sample size estimation;

$$= \frac{(Z_1\text{-}\lambda)^2 \text{ X } SD^2}{\text{Precision}}$$

$$= \frac{1.96\text{x}1.96\text{x}4.3\text{x}4.3}{0.0196 \text{ x } 0.0196}$$

=175

At 95% power, 5% absolute error, sample size was estimated to be 175. Based on this formula a sample size of 88 was obtained in each group (PRP-PCx88) and (BC-PC x 88) resulting in total sample size was **88X2=176.**

Statistical analysis:

- The parameters tested for PCs were expressed as Mean ± standard deviation (SD) and range.
- For comparison of a parameter between different types of PCs "independent t-test" was applied.
- A p-value < 0.05 was considered to indicate a statistically significant difference.
- Post hoc analysis has been done to undertake multiple comparisons for testing the mean differences among the variables.
- Pearson product- moment correlation coefficient has been used to measure the liner correlation between two sets of data.

Table 6: Investigation Schedule

Criteria	**Day 0**	**Day 5**	**Day 7**
Morphological parameters of Platelet Concentrates	✓	✓	✓
Metabolic parameters of Platelet Concentrates	✓	✓	✓
Bacteriological profile of Platelet Concentrates	✓	✓	✓
Platelet additive solution of Platelet Concentrates	✓	✓	✓
Flow cytometry study of Platelet Concentrates	✓	✓	✓
Proteomics of Platelet Concentrates	✓	✓	✓

CHAPTER 1:

IMPACT OF PLATELETS PREPARATION METHODS ON THE IN-VITRO QUALITY PARAMETERS DURING EXTENDED STORAGE PERIOD

Introduction

In 1950, William Murphy and Carl Walter invented plastics bags replacing the breakable glass bottles that were until that point and allowed evolution of a collection system capable of safe and easy preparation of multiple blood components from a single unit of whole blood.[34]

The limited shelf-life of PCs coupled with increased demand due to various causes has prompted the medical fraternity to explore various techniques of platelet collection, preparation and storage etc. Various options to suggest the optimum method for the same were considered.

The problem started with the residual Red Blood Cells (RBCs) left after the removal of PRP which were heavily contaminated with White Blood Cells (WBCs) resulting in FNHTR characterized by occurrence of formation of the micro-aggregates in the RBC which are deleterious for the patient.[34]

Currently, two methods of platelet preparation, namely, PRP and BC-PC method are widely used across the world. PRP technique is popular in North America whereas BC-PC method is widely prevalent in Europe with variable in vitro characteristics. Recent studies indicate that BC-PC is a better alternative to PRP-PC with superior quality indices, more plasma recovery and lesser risk of transfusion reactions.[34]

The underlying mechanism responsible for better acceptability of BC-PC method is due to the presence of "biologic cushion" which prevents contact activation of PCs during pellet formation. Hence BC-PC possibly experiences less stress during production than PRP-PC.[34]

Aims and objectives:

1. To compare and evaluate the viability and integrity of PCs stored in autologous plasma for an extended duration of 7 days.
2. To study the technical and quality aspect of PRP-PC versus BC-PC.
3. To study the acceptability of platelet morphological indices as quality indicator during the extended period of storage.

Materials and Methods

Following the selection of an appropriate vein, the antiseptic preparation of the selected site was done using a two steps procedure consisting of initial application of betadine followed by 70% of alcohol. The duration of the entire blood collection lasted for 5 ± 3 minutes of starting and at the rate of 50-70 ± 5ml/minute accompanied by continuous mixing with the anti-coagulant.[34]

Preparation of (PRP-PC):

WB was collected in a 450 ml triple bag containing Citrate-phosphate-dextrose solution with adenine (CPDA) 1 anticoagulant (HLL, Ltd. Puliyarakonam, Trivandrum, India). PRP –PC was separated from WB by light spin centrifugation by Heraeus 6000i, Germany refrigerated centrifuge at 1750 revolutions per minute (rpm) for 11 minutes at 21^0C, with acceleration and deceleration curves of 5 and 4 respectively and the PCs were concentrated by heavy spin centrifugation at 3940 rpm for 5 minutes at 21^0C, with acceleration and deceleration curves of 9 and 5 respectively with subsequent removal of supernatant plasma. The PC bag was left stationary with the label side down at room temperature for approximately 1 hour. (Figure 1) The PRP was frozen promptly and stored as fresh plasma (FFP) at or below -30^0C for 1 year.

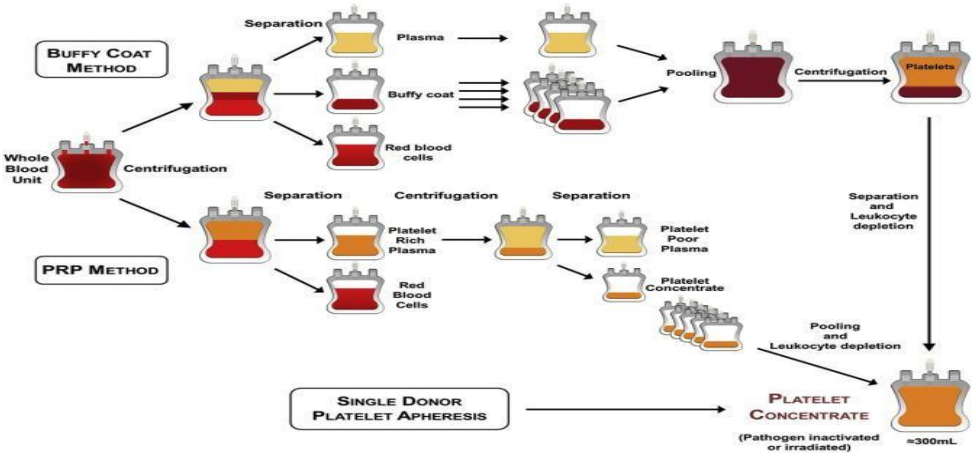


Figure 16(a): Preparation of Platelet Rich Plasma (adapted from Katharina Schallmoser 2009 :32:1-4).[35]

Method of preparation of buffy coat- platelet concentrates (BC-PC)

WB was obtained in a 450 ml of whole blood was collected in a 450-ml quadruple bag containing 63ml of CPD anticoagulant, with additive solution Saline Adenine Glucose Mannitol (SAGM), (HLL, Ltd. Puliyarakonam, Trivandrum, India). Followed by 'hard spin'

centrifugation at 3940rpm for 5 minutes at 21^{0}C with acceleration and deceleration curves of 9 and 4 respectively. Subsequently, the following by products were noted;

1. The top layer-platelet poor supernatant plasma (150-200ml) and collected into satellite bag
2. Middle layer-buffy coat, containing approximately 90% of PCs, 70% of WBC and 10% of red cells are expressed into separate bag.
3. Bottom layer –packed red cells. (refer figure-16)

Next, SAGM solution was added to the red cells obtained and stored at 4^{0}C whereas, platelet poor plasma was shifted to -40^{0}C deep freezer as fresh frozen plasma (FFP).

Following this plasma was added to buffy coat preparation and underwent "light spin" centrifugation at 1,100 rpm for 6 minutes at 21^{0}C, with acceleration and deceleration curves of 5 and 4 respectively which resulted in the final product of BC-PC being obtained and stored at RT in platelet agitator and the residual WBCs and RBCs being discarded.(refer figure-16)

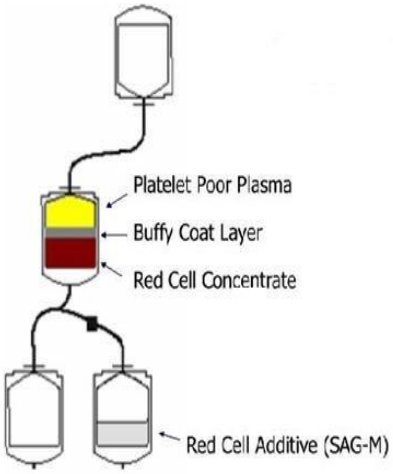


Figure 16(b): Preparation of BC-PC (adapted from Katharina Schallmoser. 2009:32:1-4).[35]

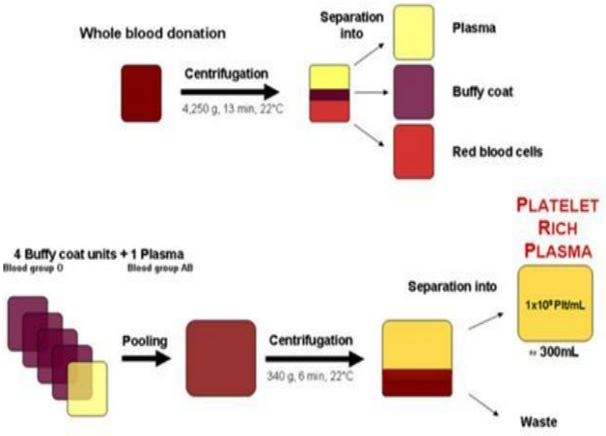


Figure 16(c): Preparation of BC-PC (adapted from Katharina Schallmoser2009:32:14).[35]

Table 7: Platelet morphological parameters (adapted from Synder et al 1983;44:300-04).[37]

Parameter	Normal values	Description	units
Mean platelet volume (MPV)	7.2 to 11.7fl	Analyzer –calculated measure of thrombocyte volume	fentoliters (FL)
Platelet volume distribution width (PDW)	8.3 to 56.6fl	Indicator of volume variability in PCs size	fentoliters (FL)
Plateletcrit (PCT)	0.22 to 0.24%	Volume occupied by PCs in the blood	Percentage (%)
Platelet larger cell ration (P-LCR)	>12fl	Indicator of larger (>12 Fl) circulating PCs	fentoliters (FL)
Immature platelet fraction (IPF)	0.3% to 8.7%	Percentage of immature PCs	Percentage (%)

In this study we will analyze the quality of different platelet concentrates prepared by different methods as per the recommended DGHS quality norms. [Table 2][37]

Table 8: Criteria for quality assessment of PRP-PC, BC-PC and apheresis-PC (DGHS technical manual, 2nd Ed.)[37]

Quality Parameters	PRP-PC	BC-PC
Volume	40-70ml	70-90ml
Swirling	Present	Present
Platelet count/bag	$>5.5 \times 10^{10}$ in 75% of unit tested	$>5.5 \times 10^{10}$ in 75% of units tested
WBC count/bag	$5.5 \times 10^{7} – 5 \times 10^{8}$	$5.5 \times 10^{7} – 5 \times 10^{8}$
pH	>6.0 on the last day of storage in 100% of units tested	>6.0 at the end of maximum days of storage in 100% of units tested

Inclusion criteria:

- All voluntary donors of age 18-60 years.
- Weight:>45 kg for RDP and >60 kg for SDP.
- Haemoglobin.12.5g/dl.
- Platelet count -$150x10^3$/ul-$250x10^3$/ul.

Exclusion criteria:

- RBCs and bacterial contamination.
- Seropositive samples.

- Donors with history of intake of antibiotics, aspirin and Non-steroidal anti- inflammatory drugs (NSAIDS) 0.5ml of PC was mixed with 4 ml of K_2 EDTA and incubated in room temperature for 60 minutes for estimation of platelet indices by utilizing a automated by an hematology cell counter (KX 21 Sysmex). EDTA helps in better monitoring of the quality Indices of the stored PCs as EDTA chelates platelet intracellular calcium. The pH was evaluated using pH indicator solution (Renkem, Ranbaxy NewDelhi).

Results:

Table 9: Comparative evaluation of quality parameters of PRP-PC and BC-PC during 0,5 and 7 days of stored PCs.

	Parameters	**0 Day**	**5th Day**	**7TH Day**
PLT Count X 10^{10}	PRPC(n=88)	6.4 + 2.2	5.4 ± 22	5.1 ±2.2
	BC (n=88)	6.4 + 2.1	6.0 +2.1	5.9 + 6.6
P value WBC X 10^6		0.999	0.166	0.418
WBC X 10^6	PRPC (n=88)	4.8 ± 0.64	4.3 ± 0.76	4.2 ± 2.1
	BC (n=88)	3.0 ± 0.5	2.2 ± 2.0	2.1 ± 0.1
P value		<0.001	<0.001	<0.001
RBC X 10^9	PRPC (n=88)	2.8 ± 2.2	2.4 ± 2.1	2.1 ± 2.6
p value	BC (n=88)	0.5 ± 2.1	1.4 ± 2.1	1.4 + 2.1
		0.4887	0.999	0.823
pH	PRPC(n=88)	7.0 ± 1.2	6.8±0.1	6.5±0.1
	BC (n=88)	7.6 ± 0.2	7.4 ± 0.4	7.0 ± 0.2
p value		0.562	0.864	0.999

In this study the platelet yield in the PRP-PC method was within the range of 6.4× 10^{10} to 5.1× 10^{10} whereas platelet yield in PC-BC was 6.4× 10^{10} to 5.9× 10^{10} respectively. A total of 90% (45/50) PRP-PC units showed compliance with the DGHS standards[37] whereas a total of 96% (48/50) PC-BC showed conformity with the DGHS standards.[37]

The mean residual leukocyte count (WBC 10^6) in PRP-PC range from 4.8× 10^6 to 4.2× 10^6 whereas mean residual leukocyte count in BC-PC was much lesser and statistically significant (3.0×10^6 to 2.1×10^6). All the units showed compliance with the DGHS standards.[38]

With regards to RBCs contamination, in PRP-PC it ranged from 2.8× 10^6 to 2.1× 10^6 whereas in PC-BC was much lesser (0.5 × 10^6 to 1.4 × 10^6) 90% (45/50) PRP-PC and 98% (49/50) showed acceptable level of RBCs contamination. In our study the mean pH during day 0 was 7.6 and was reduced to 6.5 on day 7 ($p<0.05$).

Table 10: Comparative evaluation of morphological parameter of stored PCs for 0, 5 and 7 days (KX-21 Sysmex)

Parameters	**0 day**	**5th day**	**7th day**
PRP-PC (n=88)	PRP-PC	PRP-PC	PRP-PC
Plt ($X10^9$)	471.4 4 ± 273.9	420.8 ± 230.3	410.7 ±222.0
MPV (fL)	9.0 ± 0.63	11.68 ± 0.79	13.75 ± 0.67
PDW (%)	49.9 ± 5.05	51.7 ± 6.0	53.2 ± 5.06
PCT (%)	1.7 ± 0.12	1.6 ± 0.13	1.8 ± 1.09
BC-PC (n=88)	BC-PC	BC-PC	BC-PC
Plt (x 10^9)	490 ± 384.6	440.1 ± 340.4	415.8 ±334.0
MPV (FL)	11.0 ± 0.73	11.60 ± 0.81	12.01 ± 0.7
PDW (%)	52.0 ± 6.06	53.8 ± 7.1	54.2 ± 6.08
PCT (%)	1.8 + 0.14	1.7 + 0.14	1.6 ± 1.12

Parameters such as MPV and PDW are important morphological indices which reflect alterations associated with storage. These changes are more pronounced in PRP-PC as compared to BC –PC.

For estimation of PLTs activation a battery of tests ranging from swirling test to platelet aggregometry are available. However swirling is subjective and suffers from observer bias whereas platelet aggregometry is labor-intensive and cannot be performed regularly. Hence our study explains the utility of using PCs morphological parameters such as MPV, PDW and PCT as useful screening test platelet activation because they are simple convenient and cost effective quality indicator for determining the storage lesion of PCs.

Leukocytes in PCs have a detrimental effect on the storage medium, resulting in a significant drop in pH, increase in glucose consumption, lactic acid production, and Lactate Dehydrogenase (LDH) release during storage. Leukocytes are also responsible for, Cytomegalovirus (CMV) transmission.

Fijnheer et al[39] and Raturi M. et al[40] reported residual leukocyte count per unit in PRP-PC was higher than the BC-PC. Similarly, our study also supported these findings thus highlighting the advantage of BC-PC over PRP-PC with regard to leukocyte contamination. Nearly 99% to 100% of our units showed leukocyte count which were compatible with the DGHS standards.[38]

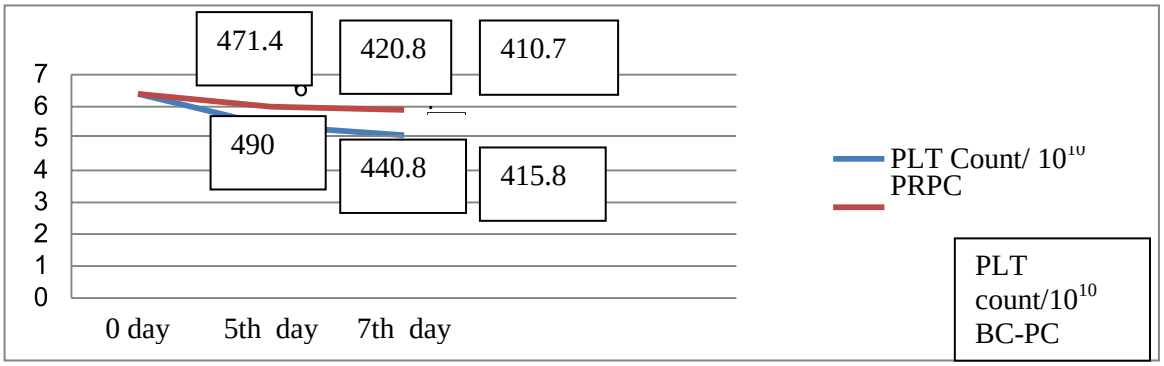


Figure 17: Line diagram showing PLT count /10^{10} with respect to time between two groups

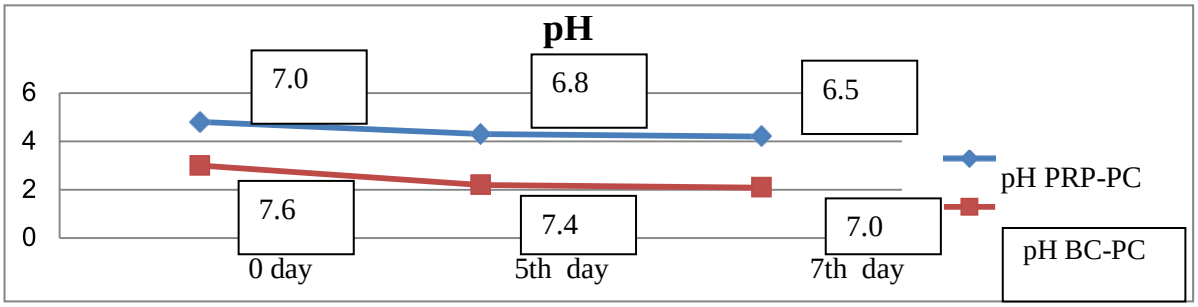


Figure 18 : Line diagram showing pH showing with respect to time between two group

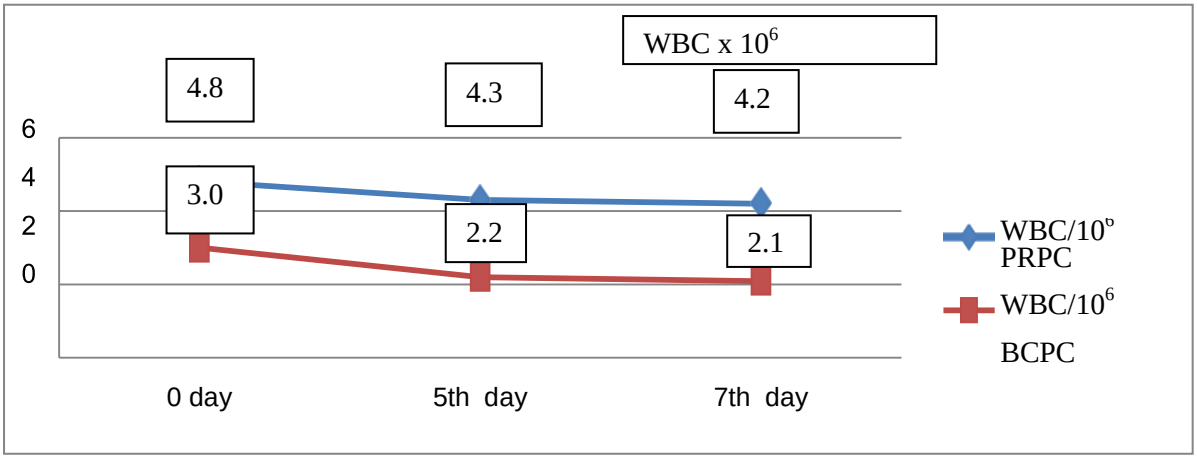


Figure 19: Line diagram showing WBC /10^6 with respect to time between two groups.

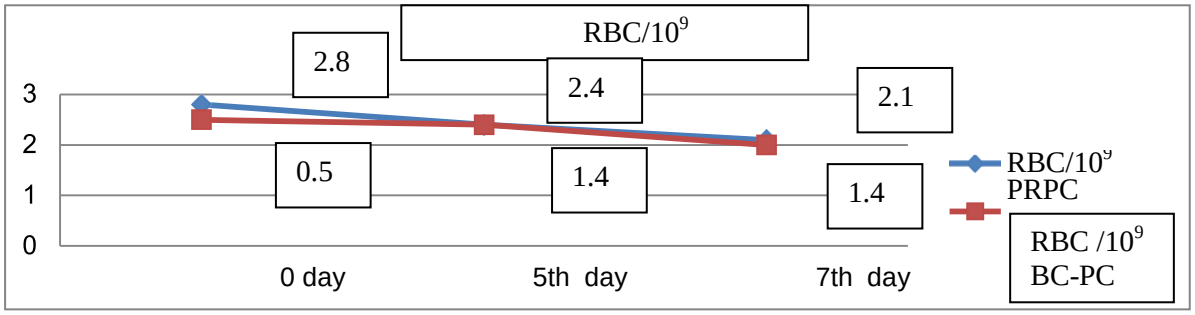


Figure 20: Line diagram showing RBC /10^9 with respect to time between two groups.

Table 11: Shows relationship between the platelet parameters and pH which were statistically significant between day 5 and day 7 of storage.

Paired Samples Test

Platelet Parameters		Paired Differences					t	Significance (2-tailed)
		Mean	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference			
					Lower	Upper		
PLT	Day 5 vs Day 7	25.302000	7.569231	1.070451	23.150848	27.453152	23.637	.000
PDW	Day 5 vs Day 7	-.337200	2.255917	.319035	-.978324	.303924	-1.057	.000
MPV	Day 5 vs Day 7	-1.093800	.362581	.051277	-1.196844	-.990756	- 21.331	.000
PLCR	Day 5 vs Day 7	-2.460400	1.031648	.145897	-2.753591	-2.167209	- 16.864	.000
pH	Day 5 vs Day 7	-.326200	.205624	.029080	-.384638	-.267762	- 11.217	.000

Paired Samples – Pearson correlation

(* Pearson correlation coefficient (r) represents strength of association between pH and other platelet indices).

Table 12: Shows that platelet indices (PLT,PDW,MPV) had a positive correlation of 436,.460,.480 respectively for 5th day and 7th day of storage showing statistical significances.

Platelet Parameters		N	Pearson correlation (r)*	Significance P value
Pair 1	PLT (5 vs 7)	50	.436	.002
Pair 2	PDW (5 vs 7)	50	.460	.001
Pair 3	MPV (5 vs 7)	50	.480	.000
Pair 4	PLCR (5 vs 7)	50	.295	.037
Pair 5	PH (5 vs 7)	50	.936	.000

Discussion:

The pathogenesis of PSL is dependent on three factors namely a) changes in the metabolic profile of PCs .b) platelet aging and senescence and c) alteration in the morphology of PCs. PSL is characterized by reduction in vivo platelet recovery, survival and reduced hemostatic function post transfusion.[41]

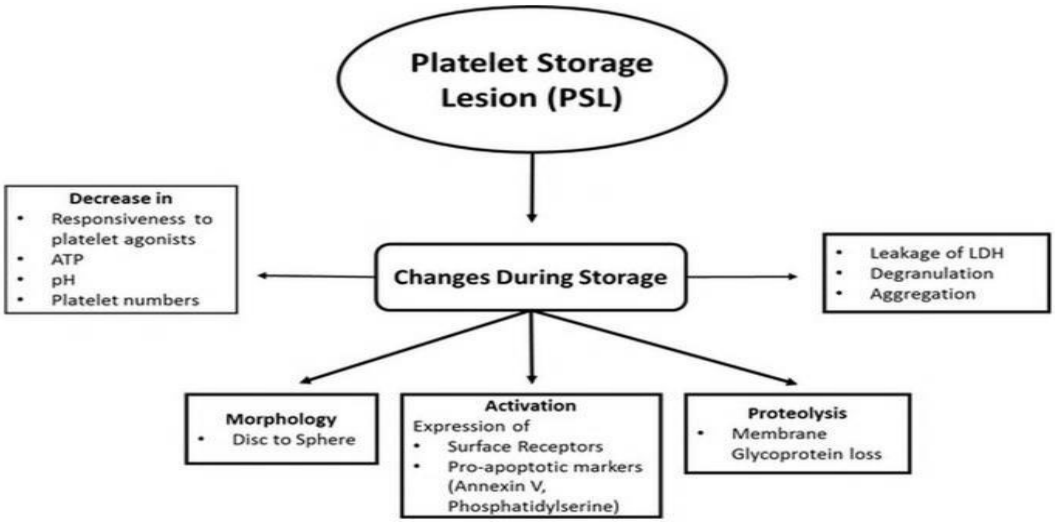


Figure 21: Pathogenesis of platelet storage lesion.(adapted from Guppy M et al 1990;59:146-152).[11]

Pre-analytical factors including donor characteristics along with the onset of PSL are responsible for inadequate platelet function which in turn poorly affects the post transfusion survival.[41]

Proper maintenance of equipment along with strict adherence to standard operating protocol are required to achieve the optimum platelet yield with proper emphasis on regulation of room temperature as cool temperature affects the structure and quality of PCs.[41]

In addition to this, there is marked variation in platelet preparing processes which includes a) methods of production b) type and amount of additive solution used c) presence/absence of leuco-reduction and d) use and type of pathogen inactivation method along with e) duration of storage period.[42]

Hence we undertook the study of comparative evaluation to study the impact of different preparation method on the in vitro quality of PCs during their extended storage period.

WB automation offers several benefits over semi-automated blood component separation techniques. The processing of blood components is considerably easier reducing the likelihood of error and shortening training time.[43] Blood centers which have adopted whole blood automation gained good logistical flexibility, along with procedural efficiency and better output.[44] Some additional benefits are also available includes: a) reduction in turnaround time (TAT)[45] b) promotion of pooling of PC leading to optimization of platelet yield.[46] c) better cell separation with less contamination of PC.[47] d) ensuring traceability of PCs.[48] e) adherence of PC to quality standards.[49]

To maintain highest quality of blood components Indian blood centers should aspire to adopt whole blood automation.[50] It offers standardization and simplification for whole blood processing when compared to semi-automated processing systems.[51]

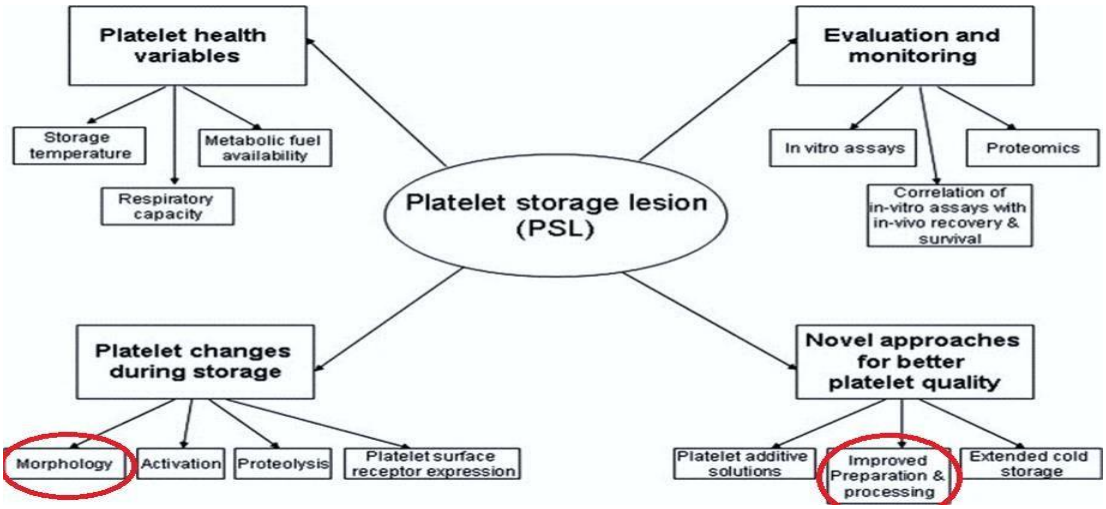


Figure 22: Various mechanism of Platelet storage lesion (adapted from Shrivastava M 2009;41:105-13)[52]

Alteration in PC indices during storage could act as helpful quality indicator of stored PCs.[53] Studies by Seghatchian et al [41] and Krailadsiri et al[41] have highlighted MPV is an vital indicator of stored PCs which is inversely related to pH, indicating a poor quality maintenance of stored PCs.[56] Identical finding were also noted with regard to PDW.[55] Similar to the findings of H. Singh et al [54] our study emphasizes that platelet indices can also be considered for effective monitoring of quality of stored PC when pH is constantly maintained within 6-7.2[57]

Conclusion:

We conclude our study regarding the comparative evaluations of impact of PCs preparation methods on the in-vitro quality parameters during extended storage period by observing the following facts: 1) increase in leuko reduction of blood components, decrease in Transfusion-Related Acute Lung Injury (TRALI) and Transfusion-associated graft-versus-host disease (TA-GVHD) adverse reaction to blood components. 2) decrease in –vitro platelet activation, possible extension of platelet storage beyond 7 days.3) better process control by semi-automated production equipment and more efficient use of staff.4) more cost- effectiveness due to increase in recovery of plasma for fractionation industry.5) the suitability of the platelet indices to act as quality indicator of stored PCs along with pH during the extended period of storage.

CHAPTER II

METABOLIC PARAMETERS OF STORED PLATELETS

Introduction:

The survival of PCs, like that of all other 1iving systems, depends on the maintenance of delicate biochemical balance between different substances including, in particular, glucose, pH and adenosine triphosphate (ATP).[60]

Storage of PC is a challenging problem which calls for immediate attention and hence many study done by Fijnheer R et al[39] have been carried out to find an ever lasting solution for the same. The pH estimation of stored platelet is considered to be one the most important criteria to estimate platelet viability and to rule out PSL.[39]

The correct determination of pH in stored PCs is absolutely essential and has been suitability in-cooperated in AABB and DGHS standards.[26] According to AABB standard pH estimation is > 6.2, and according to DGHS standard pH estimation of PC should be ≥ 6.0 respectively.[26]

PCs bags play a vital role in the maintenance of its bio-chemical hemostasis. The storage bags should have the following characteristics as shown in the figure given below,

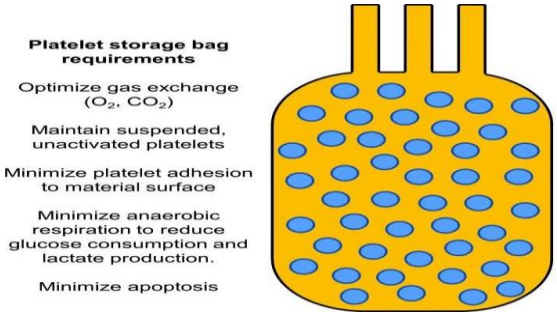


Figure 23: Essential requirements of platelet storage bag (adapted from Yuasa T et al 2004; 126:153–59).[61]

Table 13: Showing composition of blood bags (adapted from Yuasa T et al. 2004; 126:153–59).[61]

Plasticizer	Characteristics
Di ethylhexyl phthalate (DEHP)	Low gas permeability, storage up to 3 days
Tri-2 ethylhexyl trimelliate (TEHTM)	Have sufficient O_2-CO_2 permeability. Storage of PCs for at least 5 days
Butyrl tri hexyl citrate (BTHC)	Equivalent to polyolefin, affected by method of sterilization
Polyolefin (PL-732 plastic)	Higher permeability characteristics. Storage of PCs for 7 days
Ethylene-vinly acetate (EVA)	Have sufficient O_2-CO_2 permeability. Storage of PCs for at least 5 days

Aims and objectives

1. To compare and evaluate the viability and integrity of PCs stored in autologous plasma for an extended duration of 7 days.
2. To determine metabolic parameters– pO_2, pCO_2, Glucose, Lactate for an extended duration of 7 days at regular intervals.

Materials and methods

WB derived BC-PC (n=88) and PR-PC (n=88) were prepared as per the SOP.[2] The study samples were determined as per the pre-defined inclusion and exclusion criteria. Standard quality control (QC) parameters were regularly followed on day 0, 5 and 7 for PR-PC and BC-PC respectively (Refer Table 3).[26] Serial sampling was done on 0, 5 and 7 days respectively with 2ml of sample from each PC were collected aseptically from the tube segments after adequate striping.

Relevant guidelines regarding ABG estimation was followed as per the manufacturer's protocol. Sampling was done on day 5 and 7 days respectively, through sample site coupler with bacterial filter 4C2405 (Baxter, USA), and large bore needle to prevent PC activation. 5ml syringe sample was used for measurement of pH, pO_2 and pCO_2 using blood gas analyzer (Novaultra C, Nova Biomedical Corporation, USA) at 37^0C following the manufacturer's instructions.[26] The results was corrected for temperature to 22^0C. The pH meter electrode was placed in PCs and swirled in the solution.

Table 14: Reference level of metabolic parameters as per ABG analyzer.[26]

Metabolic parameters	Reference level
pO_2	75-100mmHg
pCO_2	38-42mmHg
HCO_3^-	22-28mEq/L
Glucose	70-110mg/dl
pH	7.34-7.44

Statistical analysis

All analyses were performed with the software Statistical Package for Social Sciences (SPSS 13.0) for Windows (SPSS Inc., Chicago, IL, USA).

Results

Estimation of metabolic parameters of stored PCs is essential as it provides vital information regarding oxidative and glycolytic pathways and its effect on pH maintenance as fall in pH is associated with deleterious effect on PC metabolism.

The results mentioned below in the tables highlight the findings of our study.

There was not much change in pH on day 5 and 7 when compared with day 0 values but there was statistically significant in pH between day 0 and day 7. (Table14 and Figure 24)

Table 15: pH changes from day0, 5 and 7 between PRP-PC versus BC-PC

PRP-PC (n=88)	**Mean**	**Std. Deviation**	**t value**	**p value**
Day 0	6.542	0.4150		
Day 5	5.114	0.4214	0.375	0.849
Day 7	4.962	0.5434	12.164	<0.0001**
BC-PC (n=88)	**Mean**	**Std. Deviation**	**t value**	**p value**
Day 0	7.276	0.4147		
Day 5	6.274	0.4208	0.312	0.755 (between day 0, 5 and 7)
Day 7	5.967	0.5425	11.185	<0.0001** (between day 0 and 7)

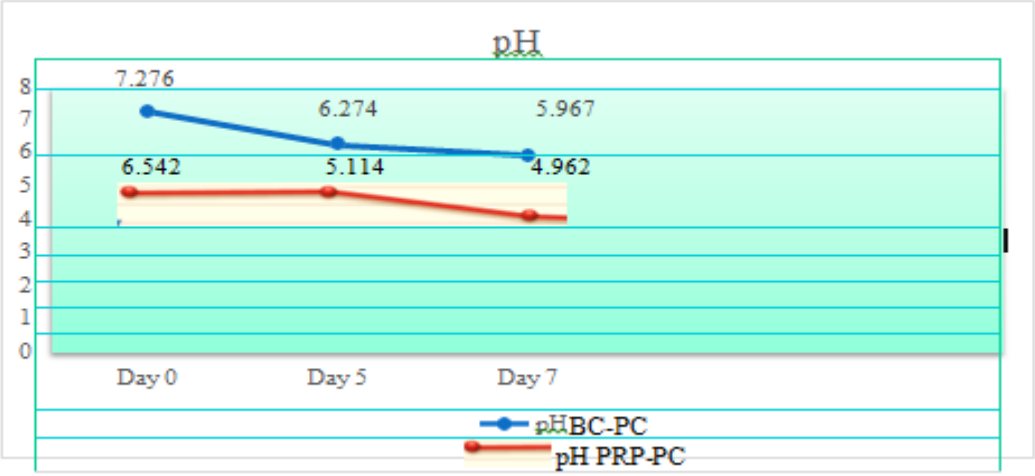


Figure 24: Line diagram showing pH changes from day0, 5 and 7 between PRP-PC versus BC-PC

Table 16: pCo_2 changes from day0, 5 and 7 between PRP-PC versus BC-PC

PRP-PC (n=88)	Mean	Std. Deviation	t value	p value
Day 0	127.6461	6.8304		
Day 5	124.652	6.8421	-14.968	>0.0001**
Day 7	119.482	6.8046	-11.762	>0.0001**
BC-PC (n=88)	**Mean**	**Std. Deviation**	**t value**	**p value**
Day 0	122.771	6.8296		
Day 5	119.556	6.8417	-13.855	<0.0001**
Day 7	117.482	6.8044	-10.661	<0.0001**

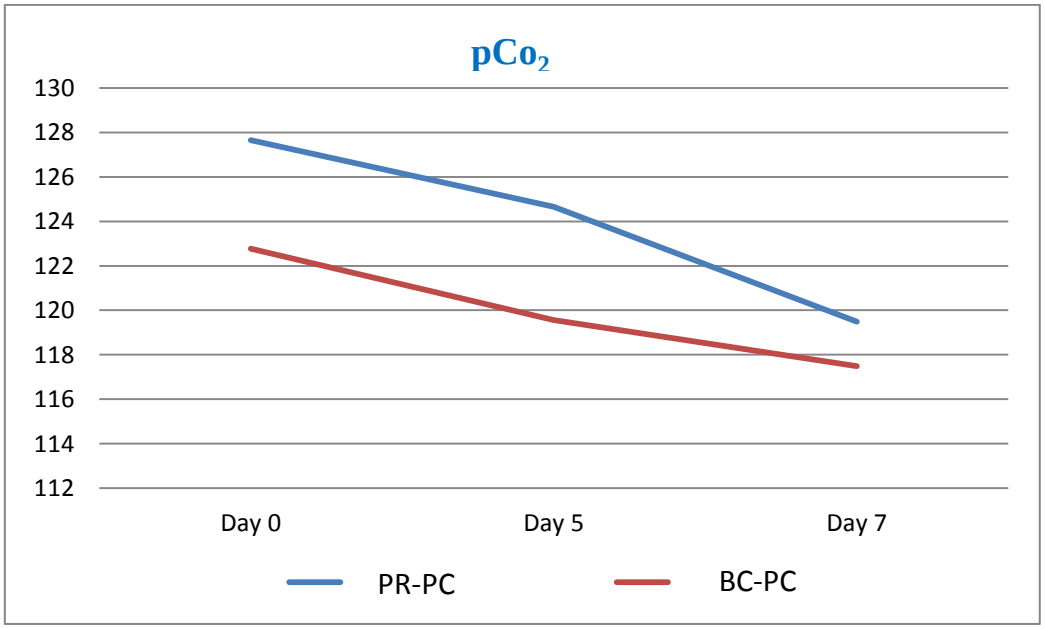


Figure 25: Line diagram showing pCo_2 changes from day0, 5 and 7 between PRP-PC versus BC-PC

Table 17: pO_2 changes from day 0, 5 and 8 between PRP-PC versus BC-PC

PRP-PC (n=88)	Mean	Std. Deviation	t value	p value
Day 0	104.762	3.78		
Day 5	112.644	4.02	-49.432	>0.0001**
Day 7	114.662	5.16	-44.025	>0.0001**
BC-PC (n=88)	**Mean**	**Std. Deviation**	**t value**	**p value**
Day 0	108.884	3.38		
Day 5	109.635	3.94	-47.332	<0.0001**
Day 7	111.848	4.14	-42.045	<0.0001**

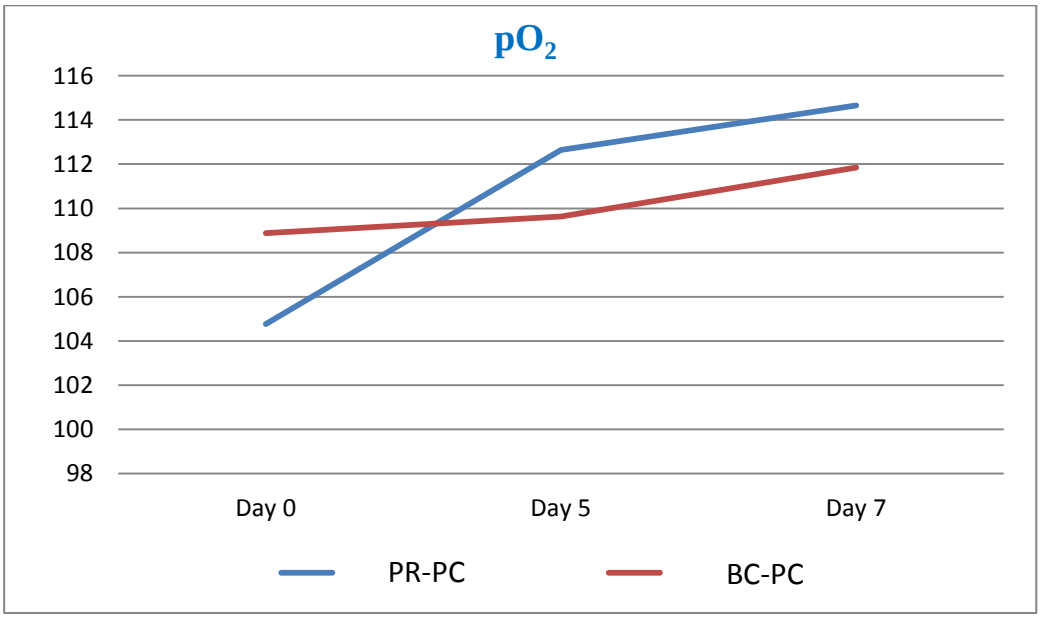


Figure 26: Line diagram showing pO_2 changes between PRP-PC versus BC-PC

Table 18: Glucose changes from day 0, 5 and 7 between PRP-PC versus BC-PC

Estimation of glucose shows gradual decrease from day 0 to day 7. (Tab 17 and Figure: 27)

PRP-PC (n=88)	**Mean**	**Std. Deviation**	**t value**	**p value**
Day 0	375.50	2.75		
Day 5	365.80	3.89	-34.252	<0.0001**
Day 7	310.09	3.69	-26.265	<0.0001**
BC-PC (n=88)	**Mean**	**Std. Deviation**	**t value**	**p value**
Day 0	392.50	2.53		
Day 5	370.60	3.76	-33.352	<0.0001**
Day 7	290.60	3.71	-27.962	<0.0001**

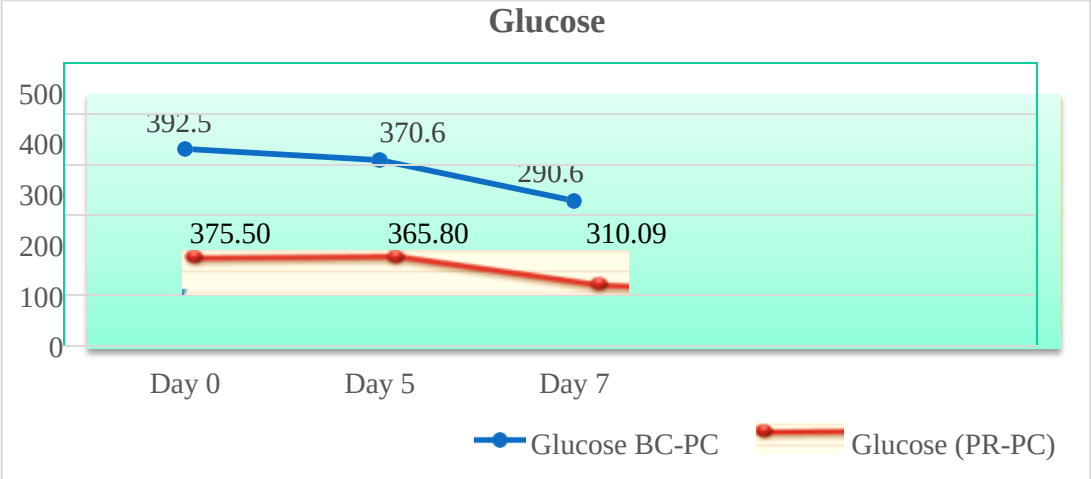


Figure 27: Line diagram showing glucose changes from day 0, 5 and 7 between PRP-PC versus BC-PC

When compared to day 0, mean Lactate levels increased on all the days. This is statistically significant on all the days. (Tab 18 and Figure: 26)

Table 19: Lactate changes from day 0, 5 and 7 between PRP-PC versus BC-PC.

PRP-PC (n=88)	Mean	Std. Deviation	t value	p value
Day 0	25.041	4.88		
Day 5	28.092	4.80	-42.235	<0.0001**
Day 7	31.048	4.90	-48.692	<0.0001**
BC-PC (n=88)	**Mean**	**Std. Deviation**	**t value**	**p value**
Day 0	22.958	4.77		
Day 5	24.080	4.76	-43.352	<0.0001**
Day 7	26.275	4.81	-47.962	<0.0001**

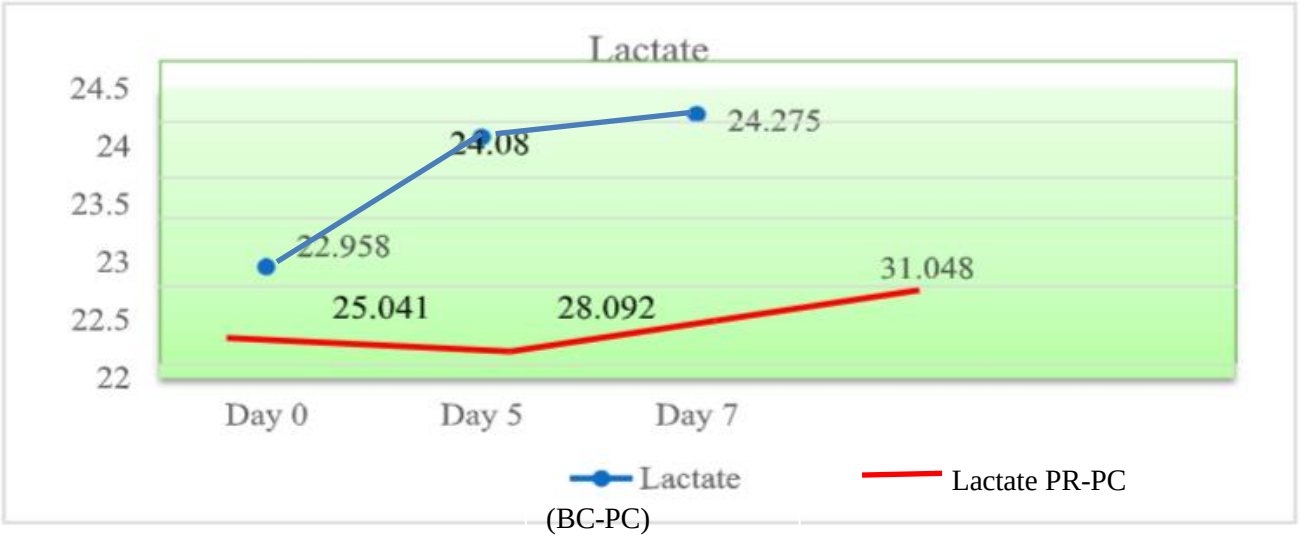


Figure 28: Line diagram showing lactate changes from day 0, 5 and 7 between PRP-PC versus BC-PC

Discussion

Cellular levels of ATP, glucose and lactate along with pH estimation offer vital clues regarding the platelet metabolic activities with the probable risk of onset of storage lesion.
Studies done Synder et al[69] and Murphy et al[70] have shown that platelet pH greater than 7.6 and lesser than 6.2 during storage correlate with decrease in vivo performance.
In order to promote gaseous exchange, support aerobic metabolism, along with maintaining optimal pH level, various interventions are necessary which includes a) increasing the size of the storage bag in order to expand the surface area b) alteration in the thickness of plastic bag to promote gaseous permeability c) encourage usage of more gas permeable plastics and/or plasticizers for manufacturing blood bags which are utilized for storage.
Along with this metabolic alteration there is increased rate of morphological alteration from disc to spheres formation as the pH attains the value of 5.7 to 5.9. Reversible morphological changes occur if the pH is maintained above 6.1 and on contrary becomes irreversible if the pH reduced below 6.1[71]

Bannai et al[72] reported that at a pH 6.85, vertical agitation responsible for alteration in platelet structure and function was less till 12 hours, but increased from 36 hours and was associated with alteration in pH level between 7.3 to 7.4 and these results shows that agitation of the sample vigorously does not get affected at low pH.
pH estimation by conventional methods has many drawbacks. Reed et al [73] have suggested an innovative method for noninvasive pH measurement by using detection with fiber optic fluorescence.

The pH alteration among the stored PCs depends on multiple factor including the types of bags used and the storage conditions. If pH falls below this level, there is a progressive rise in platelet volume and decrease in density suggesting swelling due to influx of extracellular fluid. The swelling begins at pH of 6.8 and reaches its maximum at a pH of 6.0, at which point platelet volume is increased almost two-fold. At the same time, there is an accelerated rate of disc-to- sphere transformation so that only swollen spheres are seen if pH reaches 5.7 to 5.9. These changes are almost entirely reversible if pH stays above 6.1, but they are not reversible if pH falls below 6.1.[73] These morphological observations correlate well with the results of viability in vivo. Hence, the pH level is an essential requirement for quality control of blood components. Increased PC glycolysis results in a fall of pH to levels approaching 6.0

which is associated in loss of viability. PCs become spherical, this change in shape becomes irreversible and below 6.0 the platelet metabolism ceases completely. The concentration of glucose is commonly used as a quality parameter. Fall in glucose level reflected its consumption and can be considered as an indicator for the energy generation in the cells. LDH is another parameter that was analyzed to show the extent of PC destruction during storage.[74]

During storage there is a fall in a platelet glucose level accompanied by corresponding elevation of lactate with an associated reduction in pH. The results of study shows that glucose is very essential for platelet metabolism because it acts as a substrate as glycolysis and it is also important for the tri-carboxylic acid (TCA) cycle metabolism.[65]

During glycolysis glucose is converted into lactic acid in the PCs, which in turn, lowers the pH and promotes the onset of PSL.[75] However, during TCA cycle CO_2 and H_2O are produced. This further result in reduction in platelet pH and damages the quality of PCs.[66] Identical findings were also observed by Verhoeven et al[67] who mentioned that consumption of glucose during storage is often associated with increase in lactate production.

Conclusions:

Present research endorses the following observations a) Adequacy of the storage procedure. b) suitability of the storage material used c) relevance of the quality control indicators for routine usage . This is because evaluation of pH and metabolic parameters are relatively fast and convenient. These parameters are reliable for regular platelet quality monitoring and can be effectively used as pre-release quality checks.[68]

CHAPTER III:

BACTERIAL CONTAMINATION OF PLATELETS

Introduction

Health hazards associated with platelet transfusion remains an enigma. The transfusion of blood – borne viral diseases has steadily declined whereas the clinical adversities due to bacterial contamination of PCs remain a challenge.[76]

Combined risk of all the blood borne viral infections the potential threat from bacterial contamination of PC is 50 to 250 times greater.[76] The actual incidence of bacterial contamination is 1/3000 platelet and is responsible for sepsis in 1 out of 6 contaminated products. A bacterial load of $>10^2$ CFU/ml is considered as serious risk.[77]

The common bacterial pathogen responsible for platelet contamination are *Staphylococcus epidermidis*, *Staphylococcus aureus*, *Bacillus species*, *Ecsherichia coli* in addition to bacteria from the Enterobacteriaceae group, *Pseudomonas*, *Acinetobacter species*, and *Streptococci*.[78]

The clinical expression of infection depends in the virulence of bacterial strains, the amount of bacteria transfused and the patient's immunological status. Strategies to contain platelet transfusion-associated bacterial contamination remain a priority and suggested measures include strict criteria for donor selection, proper skin disinfection and segregation of the first aliquot of blood.[79]

Aim and Objectives

It has been reported that there may be fatal sepsis in 1 out of 5,00,000 recipients due to contaminated platelet units (incidence 1% to 0.03%).[76] It is difficult to assess transfusion related sepsis due to under reporting of any actual PC contamination.

Objectives:

1. To study the incidence and pattern of bacterial contamination of stored PC.
2. To study and correlate the role of surrogate markers (pH and swirling) with bacterial contamination.

Materials and Methods

A two-step procedure for phlebotomy site preparation was performed using a povidine iodine scrub followed by application of 75% ethyl-alcohol. Sensitivity testing was done by applying chlorhexidine topically. The first 20 ml of collection is separated into a diversion pouch.[80]

WB derived PR-PC (n=88) and BC-PC (n=88) were prepared according to SOP.[2] The study samples were determined as per the pre-defined inclusion and exclusion criteria. Standard quality control (QC) parameters were regularly followed on day 0, 5 and 7 for PR-PC and BC-PC respectively (Refer Table 3). Serial sampling was done on 0, 5 and 7 days respectively with 2ml of sample from each PC were collected aseptically from the tube segments after adequate striping. Swirling was assessed as mentioned in Table 4.

Discoid platelets exposed to a light source reflect light and thus produces the "swirling" phenomenon. The principle responsible for swirling is that viable platelets in an "unactivated" state have a discoid appearance, and that shape causes light to be scattered in multiple different directions. However, platelets that are activated or are in a low pH environment, on the other hand, lose their discoid shape, and lose their light scattering abilities.[80]

The swirling effect correlates with the in vitro transformation of platelets from disk to spiny spheres. Platelets, which have undergone transformation to spheres, have very little ability to change orientation. The presence of swirling indicates pH value is within the acceptable range. The bag of the PC will be held horizontally against white light source and gently moved, so that the platelets are in motion in front of the light. In the thin areas of the bag, the appearance of swirling will be observed. (Fig.15) The degree of swirling is usually scored from 0(no swirling) to 3(maximal swirling).[26] Refer Table 4.

The pH decreases during storage depending on the stabilizer present in plastic platelet storage bags and storage conditions used. Increased platelet glycolysis results in fall of pH to levels approaching value of 6.0 in PC stored in plasma and is associated with substantial loss of viability. The majority of fresh, un-stimulated platelets are discoid with few projections. In the early observations of PCs stored at 20-24^{0}C, a gradual disc-to-sphere transformation occurs during storage.[26] The FDA approved BacT/ALERT 3D (BioMerieux, USA) was used for the study.[77] It is an automated colorimetric blood culture method, which depends on CO_2 produced by proliferating microorganism. Depending on the amount of CO_2 released, color of the pH sensitive liquid sensor located at the bottom of the bottle changes. Aseptic inoculation of 5 ml of BC-PC was done in laminar air flow hood. A positive signal lead to the concerned

PC units being blocked for issue or called back and if already transfused the concerned physician was informed about the initial positive result. Further sub-identification of the organism was done by biochemical reactions. Each PC was sampled on 0,5 and 7 days of preparation.

Results:

WB derived PR-PC and BC-PC were analyzed and those which had positive culture with micro-organism being identified on first and repeat culture were considered as confirmed positive**.**

Probable contamination i) PC units which tested positive on initial culture but negative on subsequent culture.

Negative: The PC units that did not exhibit a positive culture during the 7 days of incubation in BacT/Alert were described as negative.

Out of 88 PR-PC samples, 6 samples were positive by BacT/Alert, of which 5 were probable contamination as the repeat subsequent culture was negative. Of 88 BC-PC samples, 1 was positive and that is also probable contamination as subsequent culture was negative. The most probable reason for bacterial culture positivity could be due to improper sealing, sterile docking or contamination during the time of collection.

Table 20: Results of bacterial culture of PR-PC and BC-PC.

Sample Result	PR-PC (n=88)	BC-PC (n=88)
Confirmed Positive	1(1.13%)	0
Probable contamination*	5(5.68%)	1(1.13%)
Total positive	6(6.81%)	1(1.13%)
Total negative	82(93.18%)	87(98.86%)

Table 21: shows the distribution of results across various days of PC storage.

Sample Result	Number	Day 0	Day 5	Day 7
Confirmed Positive	01	00	01	00
Probable contamination*	06	00	03	03
Total positive	07	00	04	03

With regard to swirling, among the 88 BC-PC, 18 units (20.45%) showed grade 1, 22 units (25%) showed grade 2 and 48 units (54.54%) showed grade 3. Among the 88 PR-PC, 23

units (25.71%) showed grade 1, 33 units (38.14%) showed grade 2 and 32 units (35.42%) showed grade 3.Refer to Table 21 and Figure (line diagram)

Quality characteristics of the random-donor PCs units studies **(n =176)**

Table 22: Shows the % of PRPC and BC-PC units with respect to the standard quality characteristics. The PR-PC and BC-PC units having volumes <40 ml or >70 ml had swirling, and also their pH and platelet counts met the standard quality control criteria.

The volume of PCs (ml)	PR-PC (n=88)	BC-PC (n=88)
<40	25 (28.40%)	12 (13.63%)
40-70	33 (37.5%)	61 (69.31%)
>70	30 (34.09%)	15 (17.04%)
Swirling grade of PCs		
Grade 1	23 (26.13%)	18(20.45%)
Grade 2	33(37.5%)	22(25%)
Grade 3	32 (36.36%)	48(54.54%)
pH		
>6.4	49 (55.68%)	68(77.27%)
6.2-6.4	39(44.31%)	20(22.72%)

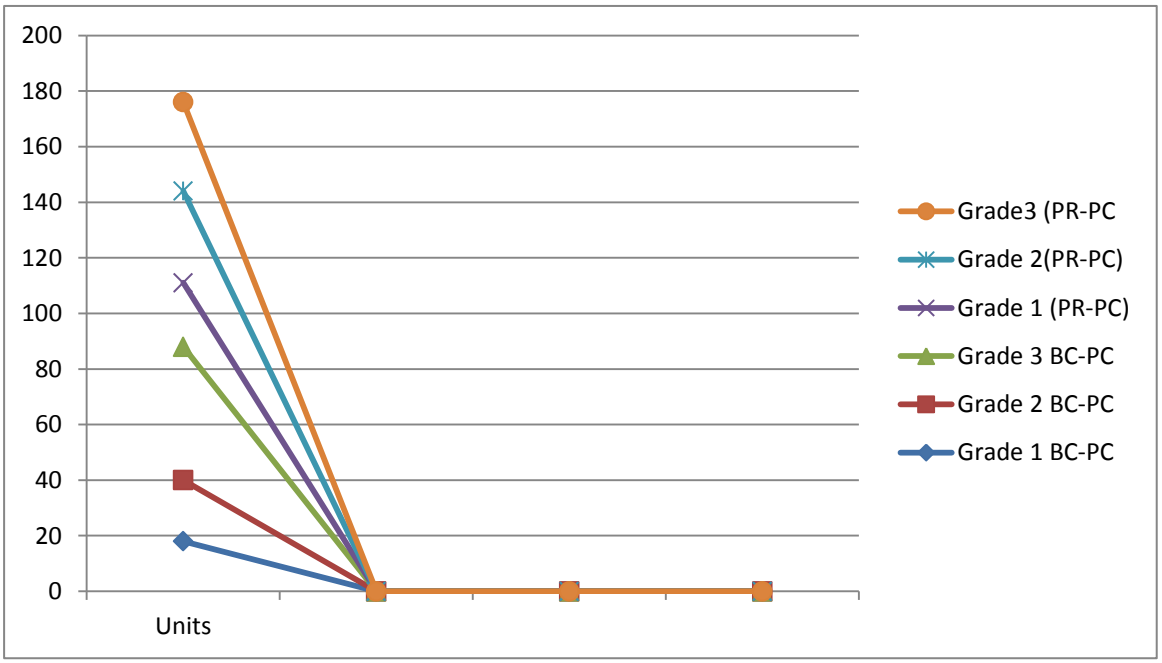


Figure 29: Shows the % PRPC of and BC-PC units with respect to the standard quality characteristics. (Swirling)

Post hoc analysis of PR-PC between swirling and other variables (multiple comparisons)

Table 23 (a): Significant difference was observed between Mean pH of PR-PC units having swirling Grade 2 and 3. Platelet counts of PR-PC units having swirling Grade 1 and 2 also showed significant statistical difference.

Grades of swirling	Mean pH	Mean platelet count ($x10^{10}$)	Volume (ml)	Statistical Comparisons
1 (16)	6.65(6.10-7.40)	6.37 (5.10-7.04)	55.30 (50.16-60.14)	p =0.001 (swirling Grade 2 vs.3) for pH
2 (26)	6.45(6.10-7.40)	6.15 (5.10-7.04)	55.15 (50.16-60.04)	p = 0.035(swirling Grade 1vs.2) for platelet count.
3 (52)	6.02(6.10-7.40)	6.04(5.10-7.20)	55.13 (50.16-60.04)	
Total (88)	6.63(6.10-7.40)	6.37(6.10-7.20)	55.31(50.16-60.04)	

Post hoc analysis of BC-PC between swirling and other variables (multiple comparisons)

Table 23 (b): Significant difference was noted between mean pH of BC-PC units having swirling Grade 2 and 3 and also observed significant statistical difference between platelet counts of BC-PC units having swirling Grade 1 and 2.

Grades of swirling	Mean pH	Mean platelet count ($x10^{10}$)	Volume (ml)	Statistical comparisons
1(42)	6.72 (6.39-7.05)	6.88 (5.25-8.51)	50.15 (37.81-62.49)	P=0.037 (swirling Grade 1 vs. 2) for platelet count
2(28)	6.77 (6.42-7.12)	6.46 (5.16-7.76)	50.31 (38.84-61.48)	
3(18)	6.64 (6.29-6.99	6.53 (5.24-7.82)	52.52 (42.19-62.85)	P=0.001 (swirling Grade 2 vs. 3) for pH
Total (88)	6.70 (6.35-7.05)	6.58 (5.2-7.96)	51.27 (40.06-62.48)	

Table 24 a: Pearson product- moment correlation coefficient to assess the relationship between the quality variables of PR-PCs.

Variables	pH (p)	Platelet count (P)	Volume(p)
pH	-	-0.12* (0.005)	- 0.02 (0.06)
Platelet count	-0.12* (.005)	-	0.06 (0.2)
Volume	- 0.02 (0.06)	0.06 (0.2)	-

Table 24 b: Pearson product- moment correlation coefficient to assess the relationship between the quality variables of BC-PCs.

Variables	pH (p)	Platelet count (P)	Volume(p)
pH	-	-0.11* (0.004)	- 0.01 (0.05)
Platelet count	-0.11* (.004)	-	0.05 (0.1)
Volume	- 0.01 (0.05)	0.05 (0.1)	-

Table 24 (a) and 24 (b) shows the correlation of pH with platelet count along with volume of PR-PC and BC-PC. There was a weak correlation between the variables in both the categories respectively.

Discussion:

Detection of bacterial contamination among the PCs remains a serious issue because of the following reasons: a) Bacteria at very low concentration can proliferate to a very significant level while in the storage period of 5 days. b) bacterial detection calls for development of diagnostic tools which can detect various bacterial species having different growth pattern and c) lack of rapid and highly sensitive diagnostic tests at time of issue.[81]

Proper skin cleaning is essential to cut down the risk of bacterial contamination due to commensal bacteria.[82] Identical observation were also noted by Wagner et al.[83] The contamination rates of PC units existing literature show a certain degree of variabilities in relation to the detection system used, time of sample taken, sample volume taken from the PC unit, and also the volume inoculated into the culture bottle.[84] Most literature is based on culture methods, but in few instances both anaerobic and aerobic bacteria were cultured.[85] Multiple reasons are responsible for variation in volume which calls for adherence to proper standards and strict monitoring of routine preparation techniques along with adequate training of technical staffs. The same observation was also highlighted by Dwivedi et al.[86] During routine practice ABO incompatible BC-PC are regularly issued without performing iso-agglutinin titers for group O which may lead to the risk of having minor incompatibility associated hemolytic transfusion reaction particularly if the donor has high titer anti-A and anti-B iso-agglutinins. Hence, performing of isoagglutinin titers for group O donors should be regularly incorporated in the routine practices in order to ensure safe transfusion services.

Minimal amount of contaminating RBCs will be invariably detected in BC-PCs even in the most refined preparation which can potential immunize an RhD（negative) recipient. The presence of RBCs is deleterious because it promotes the onset of PSL.[87] However, Beutler and Kuhl et al[88] found that low RBC and WBC count have no significant effect on platelet metabolism including the glucose consumption, lactate production or fall in pH.[88]

As per established quality standards PCs should have a pH $\geq$ 6 as pH level is the simplest indicator of onset of underlying PSL and also an essential quality indicator which reflects the viability and potential recovery of PCs after completion of storage period. PCs must be stored in adequate plasma having bicarbonate as a buffer to maintain pH $\geq$ 6 because platelet viability is significantly affected by pH, as depletion of bicarbonate by high lactic acid level typically at 20-25 mmol/l lowers pH and results in loss of platelet viability.[88]

Swirling reflects the pH level of stored PCs at RT. When PCs are stored at RT, Lactic and other acids are produce with the consequent decrease in pH level as the buffering action of plasma gets exhausted. PC viability will be adversely affected if the pH decreases to a level of pH 6.0 and below.[26] Similarly, a fall in pH can also occur due to bacterial contamination if the organisms produced acid as an end product.[26]

Visual signs of bacterial contamination can be observed by swirling but it is highly subjective procedure and hence better alternatives, such as surrogate estimations of pH, glucose, along with automated bacterial detection system (Bact/BacT/ALERT) have been developed. Although, swirling can be considered as a simple non-invasive method for conforming platelet viability but it has extremely low sensitivity and specificity.[26] However, swirling is still in practice in many resource constrained set up as it is easy to perform, economical and can be used at the time and point of transfusion.

Current study noted a positive correlation between pH and PCs (of both BC-PC and PR-PC), and identical findings were also noted on both the categories PCs (of both BC-PC and PR-PC) even with regard to platelet count. Positive correlation between PCs (both BC-PC and PR-PC) with pH value of 0.037.

Although several diagnostic tool are available for detection of bacterial contamination among the PCs due to lack of proper sensitivity and specificity along with legal technical and economic factors.[89]

In rural and resource constraint set up various non-culture methods including pH estimation , glucose assessment along with Gram staining are done which unfortunately do not provide diagnostic accuracy as culture based methods are considered as standard diagnostic method.[90]

Rapid diagnostic tools based on immunofluorescence and molecular techniques cannot be routinely applied because of economic constaints.[91]

The findings of present study proves this suitability of Bact/ALERT automated culture system for regular use in order to comply with the quality aspects and fulfill the transfusion safety standards as per the hemovigilance requirements.[92]

In order to improve TAT time with regard to detection of bacterial contamination of PCs and for improving the care of the patient's the feasibility of applying rapid test using 1ml of PCs as an adjunct to the gold-standard culture method needs to be explored. AABB mandates that every establishment can device their respective measures as per local necessity in order to minimize the risk of bacterial contamination among the PCs.[93]

The widely used BacT/Alert is a colorimetric culture method based on the detection of carbon dioxide (CO_2) produced by micro-organisms with no full proof guarantee against false negative reactions. In addition, the Heamometics e-BDS (Pall corporation, USA) detects bacterial growth by the drop in oxygen (O_2) levels in the media which is applicable for aerobic bacteria. Of late, a rapid bacterial detection test has been developed which can identify aerobic and also anaerobic Gram-positive and Gram–negative bacteria. However, due to lack of sensitivity and specificity, spot test can be only used as "adjunct" to the various automated culture method.[94]

Recently (matrix-assisted laser desorption ionization time-of-flight mass spectrometry) MALDI-TOF MS as it is been used for reliable bacterial identification from colonies in a short span of time and at an economical rate. In addition, MALDI-TOF MS enables direct identification of micro-organisms from blood cultures and urine samples.[95]

However, routine visual examination of BC-PC is still considered to be relevant and is useful to rule out discoloration, clumping or abnormal morphology. Swirling test is a useful routine procedure which can be co-related with culture reports for their predictive value with regard to contamination and is scored as follows: scoring 0: homogenous turbidity in all parts of the bag with no change with pressure, scoring 1: swirling in only in some part of the bag and is not clear, scoring 2: clear homogenous swirling in maximum portion of the bag**,** scorning 3: very clear homogenous swirling in all part of the bag.[96]

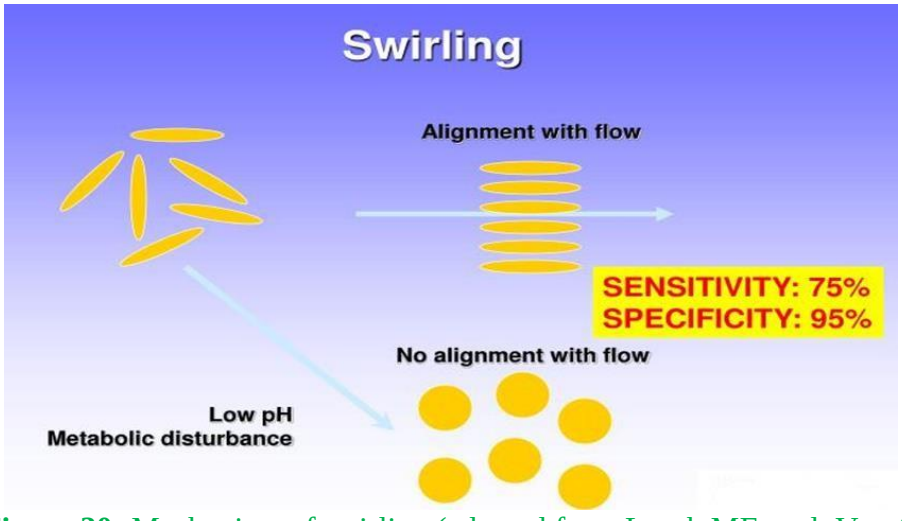


Figure 30: Mechanism of swirling (adapted from Leach MF et al. Vox Sang 1998;74(1)1180).[97]

Highly encouraging results obtained from (MALDI-TOF MS) which were characterized by reproducibility over time with a predictive value of 100%. Detecting bacteria in platelet concentrates using the MALDI-TOF approach and analyzing spectra with the platelet software present the advantages of combining the accuracy of results and sufficient sensitivity (10 c.f.c.ml^{-1}) .[98] More scientific investigations needs to be conducted to compare this novel method with the current conventional method in order to validate our results, the objective being to mitigate transfusion of PC induced bacterial contamination.[99]

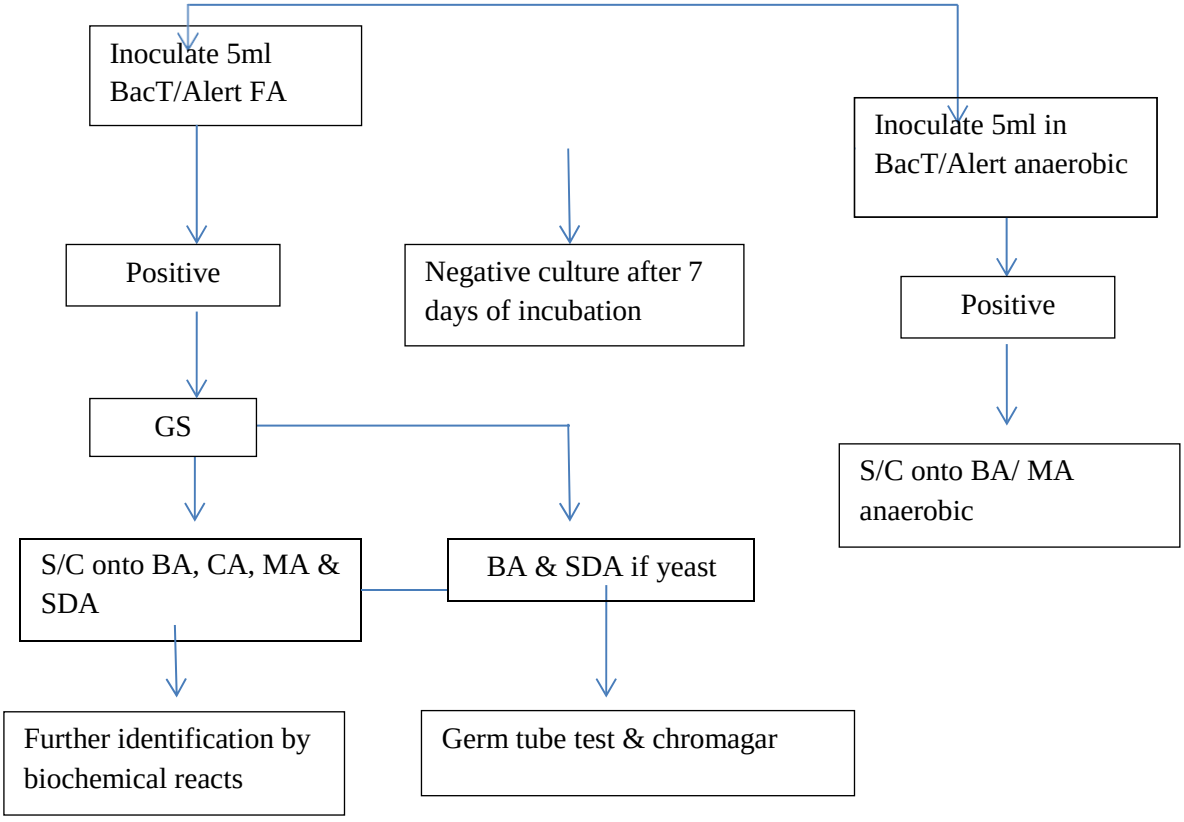


Figure 31: Flow chat regarding detection of bacteria in BC-PC Abbreviations; CA, Chocolate Agar,; MA, MacConkey Agar; BA, Blood Agar; SDA, Sabouraud Dextrose Agar (adopted from Leach MF et al. 1998;74:1180-4).[97]

Summary

Data on platelet contamination and bacterial sepsis after contaminated platelet transfusion are underreported in India. In the year 2011 Kaufman RM et al [98] reported five cases of bacterial sepsis after transfusion of bacterial- contaminated PC units. Three out of those five patients ultimately died because of bacterial sepsis.[98]

Alteration in the pH values, oxygen utilization and the level of glucose consumption are some of the relatively absolute procedures which may help in identification of bacterial proliferation in the PCs. However, these methods fail to detect the bacteria and spores at low concentration. Moreover, these methods are highly susceptible to instrumental and sampling errors coupled with prolonged (TAT) associated with loss of product during sampling procedure.[99]

The AABB's standards for blood banks and transfusion services require AABB-accredited facilities that have "methods to limit and to detect or inactivate bacteria in all platelet components". These strategies include a) preventing contamination during blood collection.
b) testing methods for platelet bacterial contamination by culture based c) secondary rapid detection methods d) pathogen reduction/inactivation technologies.[100]

Despite the availability of various "state of the art" diagnostic facilities, a final consensus on the measures to be taken towards this end is yet to be reached on a global scale. Even though pathogen reduction technologies (PRT) are being increasingly available they are not particularly effective against bacterial spores and emerging pathogens including facultative anaerobic and fastidious bacteria. Hence more efforts must be made to meet this challenge adequately and appropriately.[101]

CHAPTER IV: PLATELET WITH ADDITIVE SOLUTIONS

Introduction

PCs play a very important role in hemostasis. PCs are usually separated from whole blood. They are stored in donor plasma at 22^0C for transfusion therapy. Several studies showed that PCs maintain an adequate function for 5 days and thereafter a progressive loss of structural and functional integrity among the stored PCs leading to the onset of PSL.[102]

PSL have a deleterious effect on post transfusion efficacy of the PCs. Among all the platelet indices the evaluation of MPV is vital as MPV reflect the morphological changes that occur during the storage period. Similarly, swirling is accepted as a better alternative for the assessment of shape change and absence of swirling is predictive of poor post-transfusion increments. PCs that retain their shape in vivo at the time of transfusion are expected to be functionally better in vivo. PCs stored in PAS have been demonstrated to have a reduced risk for adverse reactions and also result in a lower incidence of other plasma associated transfusion reactions.[103]

The current study was done to assess the changes of the in vitro parameters of stored PC beyond 5 days in presence and absence of PAS. BC-PCs with prolonged shelf life will help to meet logistics support of increased availability of PCs for clinical transfusion**.**

Aim and Objectives

The aim and objective of the study were:

1. To study and compare the various morphological PCs of platelets with and without PAS on days 0, 5, 7.
2. To study and compare the pH values and cytokines of PCs with and without PAS on days 0,5, 7.

Materials and Methods:

Random donor platelet preparation:

WB derived PR-PC (n=88) and BC-PC (n=88) were prepared as per the SOP.[2] The study samples were determined as per the pre-defined inclusion and exclusion criteria. Standard quality control (QC) parameters were regularly followed on day 0, 5 and 7 for PR-PC and BC-PC respectively (Refer Table 3). Serial sampling was done on 0, 5 and 7 days

respectively with 2ml of sample from each PC were collected aseptically from the tube segments after adequate striping.

Pooling of PCs (BC-PC and PR-PC units) and ABG analysis were done as per the standard instructions obtained from the manufacturer with the ABG analyzer results being modified with respect to temperature at 22^0C. During storage at RT the PC units were kept in platelet incubator (Thermopenpol) having a) constant agitation at 70 cycles per minute.

For storage of PCs in PAS, 8ml of BC-PC and 10-15 ml of plasma was left with the PC, an expected final concentration was 80% additive solution and 20% plasma. The volume of additive solution and stored PCs had a mean volume of PAS and stored platelet 50± 1ml. Solutions of PAS consists of 5.26 gm sodium chloride, 5.02 gm sodium gluconate, 2.22 gm sodium acetate anhydrous, 0.373 gm potassium chloride, 0.305 gm magnesium chloride hexahydrate, 3.213 gm sodium citrate.(Macopharma India Transfusion Solution Private Limited, Span Health Care Private Limited).(Refer Table 25)

Immediately after preparing the PR-PC and BC-PC about 5 ml sample was removed for quality control and for evaluation of cytokines including Interleukin-1 and TNF-α were assessed in the stored platelet supernatants utilizing commercially available assays (BioSource International Inc., Camarillo, CA, USA) in accordance with manufacturer's protocol. The minimum detection limits were 1.5 pg/ml for IL-1 and 10pg/mL for TNF- α.

Results:

Comparisons between groups were analyzed using the student t-test for independent samples. Results were expressed as mean values and 95% confidence intervals. P-value below 0.05 were considered statistically significant. Data were entered into Microsoft Excel and analyzed using IBM SPSS Statistics for Windows, Version 21.0., 2013 (IBM Corp., Armonk, NY, USA)

Table 25: Various components of multiple PAS solution.(adapted from Ringwald J,Transfus Med Rev 2006;20:158-64).[104]

Table of Platelet Additive Solutions

New Name	Citrate	Phosphate	Acetate	Magnesium	Potassium	Gluconate	Glucose	Alternate Names	Previous ISBT 128 Name
PAS	NS	NS	NS	NS	NS	NS	NS		Not named
PAS-A	X	X			X			PAS (1)	Not named
PAS-B	X		X					PAS II, PAS-2, SSP, T-Sol	PASII
PAS-C	X	X	X					PAS III, PAS-3, Intersol	PASIII
PAS-D	X		X	X	X	X		Composol PS	PAS IIIMgK (note, Composol PS should not have been called PASIIIMgK)
PAS-E	X	X	X	X	X			PAS IIIM, SSP+	Not named
PAS-F			X	X	X	X		PlasmaLyte A, Isoplate	Not named
PAS-G	X	X	X	X	X		X		Not named

Table 26: Chemical composition of PAS III along with the function of various chemicals. (adapted from Cohn CS, Transfus 2014;54:1927-34)[105]

PAS III: Chemical Composition	
Components	Action
	Effects on PCs metabolism
Acetate	• Substrate for platelet metabolism (with glucose) • Maintains pH Stable (storage)
Phosphate	• pH buffer • Maintaining good in vitro characteristics during

	interruption of agitation
Effects on the function of PCs membrane	
Citrate	• Prevention of coagulation
Magnesium	• Prevention of aggregation • Reduction of PCs activation
Potassium	• Prevention of aggregation • Reduction of PCs activation • Reduction of glycolysis • Maintaining pH levels

Estimation of platelet count for PR-PC and BC-PC

Table 27: Comparative table of platelet count in presence and in absence of PAS for PR-PC and BC-PC respectively. There was no substantial difference in mean platelet count from Day 0 till Day 7 of follow up.

Storage Period	**Group PR-PC (n=88)**				**P value**
	Platelet count Without PAS (n=44)		**Platelet count with PAS (n=44)**		
	Mean	**SD**	**Mean**	**SD**	
Day 0	428	148.7	423.4	141.2	0.652
Day 5	433.9	171.3	430.2	128.5	0.712
Day 7	460.9	187.6	398.6	164.5	0.058
Group BC-PC (n=88)					
Storage Period	**Platelet count Without PAS (n=44)**		**Platelet count with PAS (n=44)**		**P value**
	Mean	**SD**	**Mean**	**SD**	
Day 0	478	156.7	468.4	192.3	0.659
Day 5	473.9	192.7	465.2	221.6	0.734
Day 7	463.9	189.4	420.6	199.3	0.074

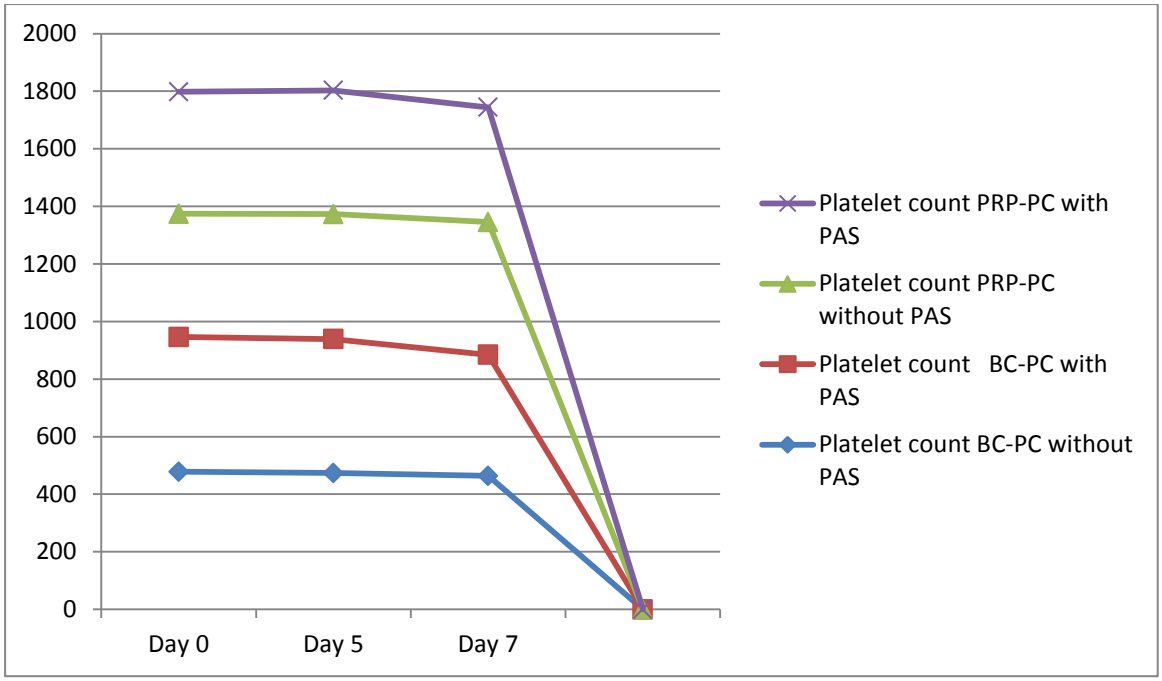


Figure 32: Comparative study of platelet count accompanying PAS and in absence of PAS for BC-PC and PR-PC.

Estimation of MPV for PR-PC and BC-PC

MPV is a analyzer – calculated measurement of thrombocyte volume and expressed as femtoliters[11]

Table 28: Comparative study of MPV of PCs accompanying PAS and not accompanying PAS .There was remarkable differences in MPV from Day 0 till Day 7 of follow up.

Storage Period	Group PR-PC (n=88)				P value
	MPV without PAS (n=44)		MPV with PAS (n=44)		
	Mean	SD	Mean	SD	
Day 0	5.1	1.2	3.25	3.5	0.764
Day 5	13.2	1.4	5.16	1.7	<0.01*
Day 7	16.4	1.6	7.9	2.2	<0.001*
Group BC-PC (n=88)					
Storage Period	**MPV without PAS (n=44)**		**MPV with PAS (n=44)**		**P value**
	Mean	**SD**	**Mean**	**SD**	
Day 0	3.9	1.1	4	3.1	0.888
Day 5	12	1.5	4.8	1.5	<0.001*
Day 7	14.5	1.7	5.4	1.6	<0.001*

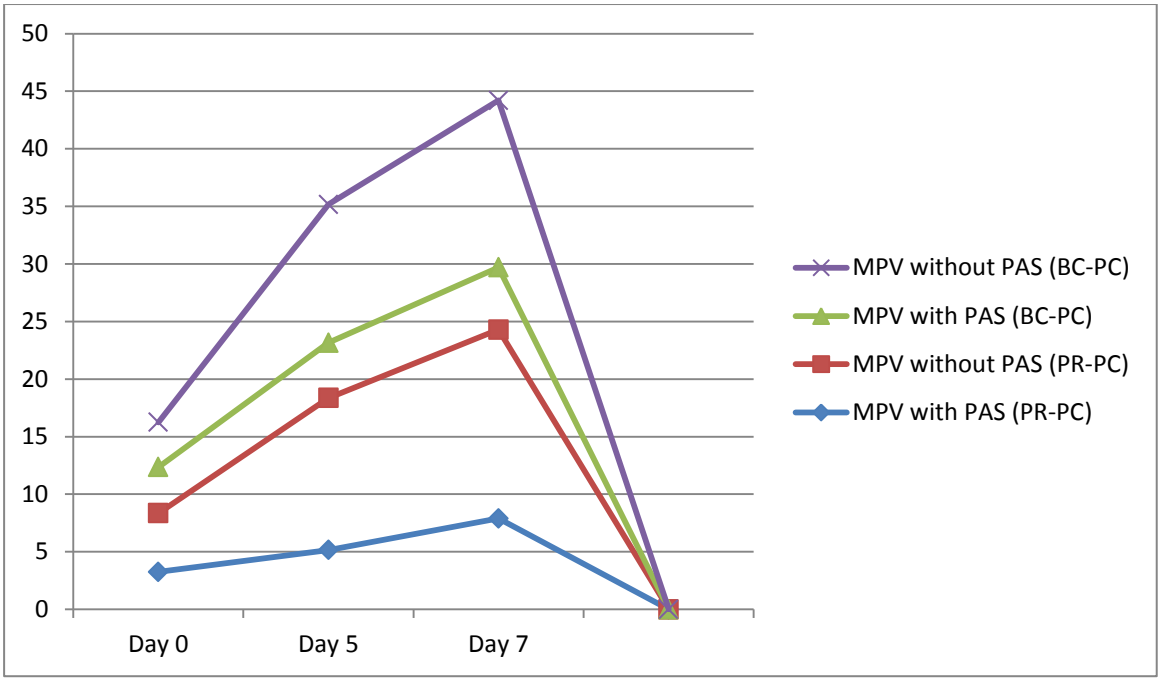


Figure 33: Comparative study of MPV of PCs with PAS and without PAS for PR-PC and BC-PC.

Estimation of PDW for PR-PC and BC-PC

Table 29: Estimation of PDW of PCs in presence and absence of PAS-There was substantial differences in PDW between two methods at from Day 0 till Day 7.
PDW which is indicator of volume variability in PCs size and expressed as percentage (%).

Storage Period	Group PR-PC (n=88)				P value
	PDW without PAS (n=44)		PDW with PAS (n=44)		
	Mean	SD	Mean	SD	
Day 0	16.3	1.6	15.3	1.7	0.321
Day 5	25.5	2.4	17.8	1.9	<0.001*
Day 7	26.8	3.1	19.2	2.2	<0.001*
Group BC-PC (n=88)					
Storage Period	**PDW without PAS (n=44)**		**PDW with PAS (n=44)**		**P value**
	Mean	**SD**	**Mean**	**SD**	
Day 0	14.4	1.7	14.2	1.6	0.267
Day 5	21.2	2.9	16	2.6	<0.001*
Day 7	21.5	1.5	17.3	3.5	<0.001*

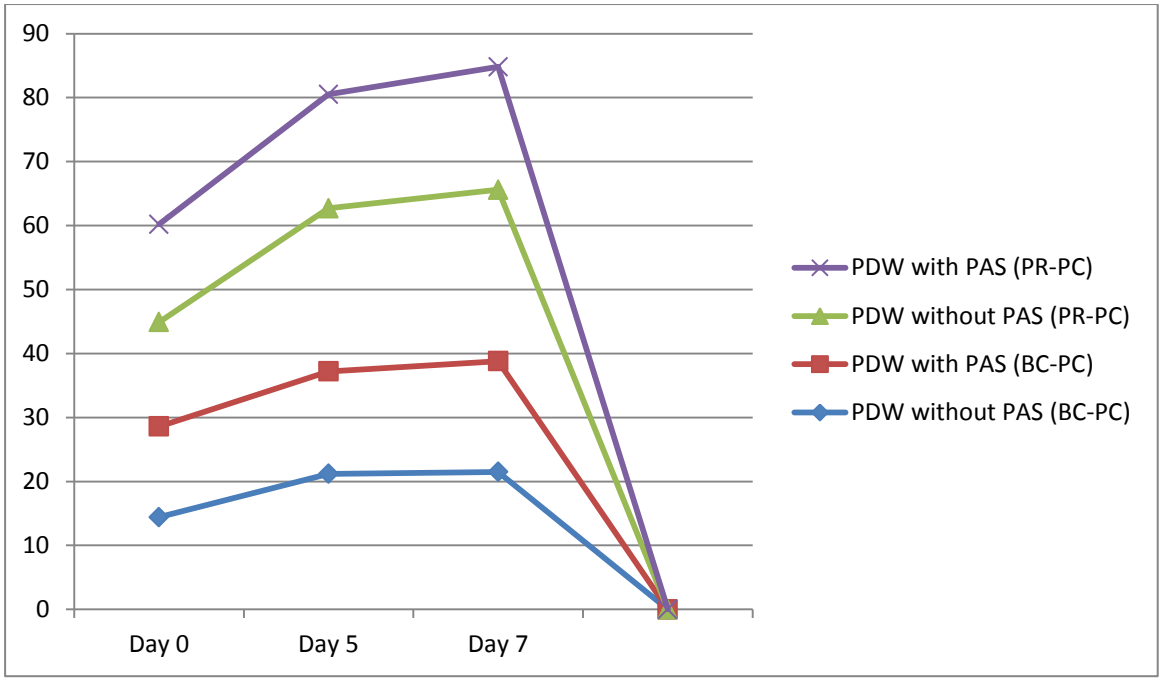


Figure 34: Showing PDW comparison of PCs in presence and absence of PAS for PR-PC and BC-PC respectively.

Estimation of P-LCR

Platelet larger cell ratio (P-LCR)[11] is indicator of larger (> 12Fl) circulating PCs and expressed as percentage

Table 30: Comparison of P-LCR PCs in absence and presence of PAS:-There was noteworthy differences between PR-PC and BC-PCs without and with PAS on different days of storage.

Storage Period	Group PR-PC (n=88)				P value
	PLCR without PAS (n=44)		PLCR with PAS (n=44)		
	Mean	SD	Mean	SD	
Day 0	15.9	1.3	13.9	1.5	0.092
Day 5	28.2	1.5	20.6	1.7	<0.001*
Day 7	31.6	1.7	22.9	1.9	<0.001*
Group BC-PC (n=88)					
Storage Period	**PLCR without PAS (n=44)**		**PLCR with PAS (n=44)**		**P value**
	Mean	**SD**	**Mean**	**SD**	
Day 0	13.7	1.2	12.6	1.4	0.089
Day 5	25.4	1.6	18	1.6	<0.001*
Day 7	29.8	1.8	21	1.7	<0.001*

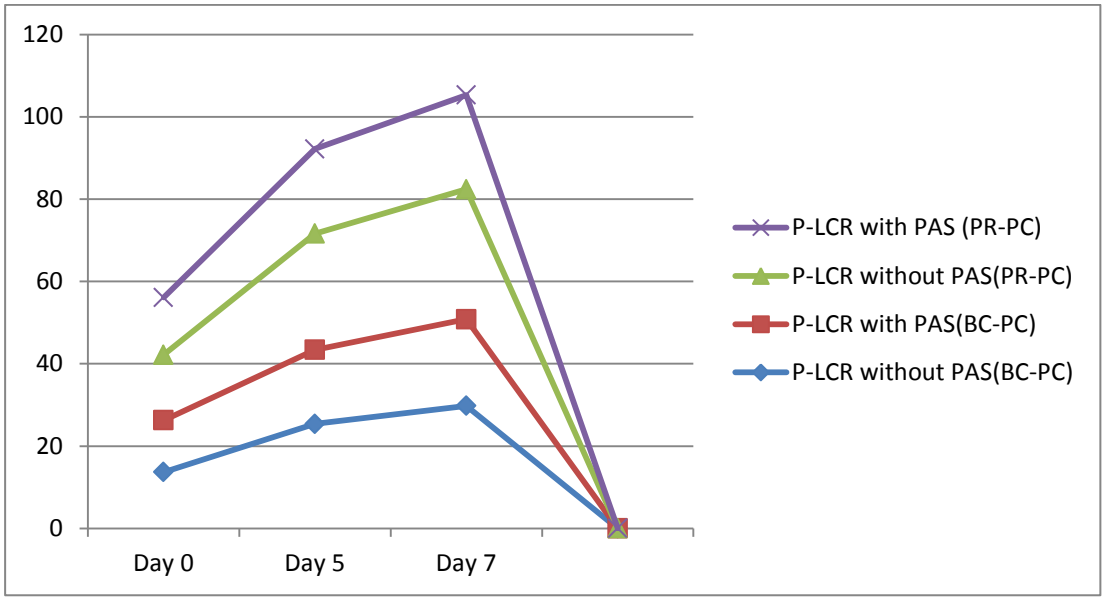


Figure 35: Comparison of P-LCR of PCs in presence and absence of PAS for PR-PC and BC-PC respectively.

Estimation of pH for PR-PC and BC-PC

Table 31: Comparison of pH of PCs with and without PAS for PR-PC and BC-PC. There was significant statistical differences in pH between two methods from day 0 till day 7 follow up.

Storage Period	Group PR-PC (n=88)				P value
	pH without PAS (n=44)		pH with PAS (n=44)		
	Mean	SD	Mean	SD	
Day 0	7.4	0.6	6.9	4.9	0.321
Day 5	9.1	0.5	6.3	0.6	<0.001*
Day 7	9.7	0.7	7.1	0.6	<0.001*
Group BC-PC (n=88)					
Storage Period	**pH without PAS (n=44)**		**pH with PAS (n=44)**		**P value**
	Mean	**SD**	**Mean**	**SD**	
Day 0	6.4	0.4	6.7	4.7	0.291
Day 5	8.6	0.5	6.5	0.4	<0.001*
Day 7	9.1	0.4	6.5	0.4	<0.001*

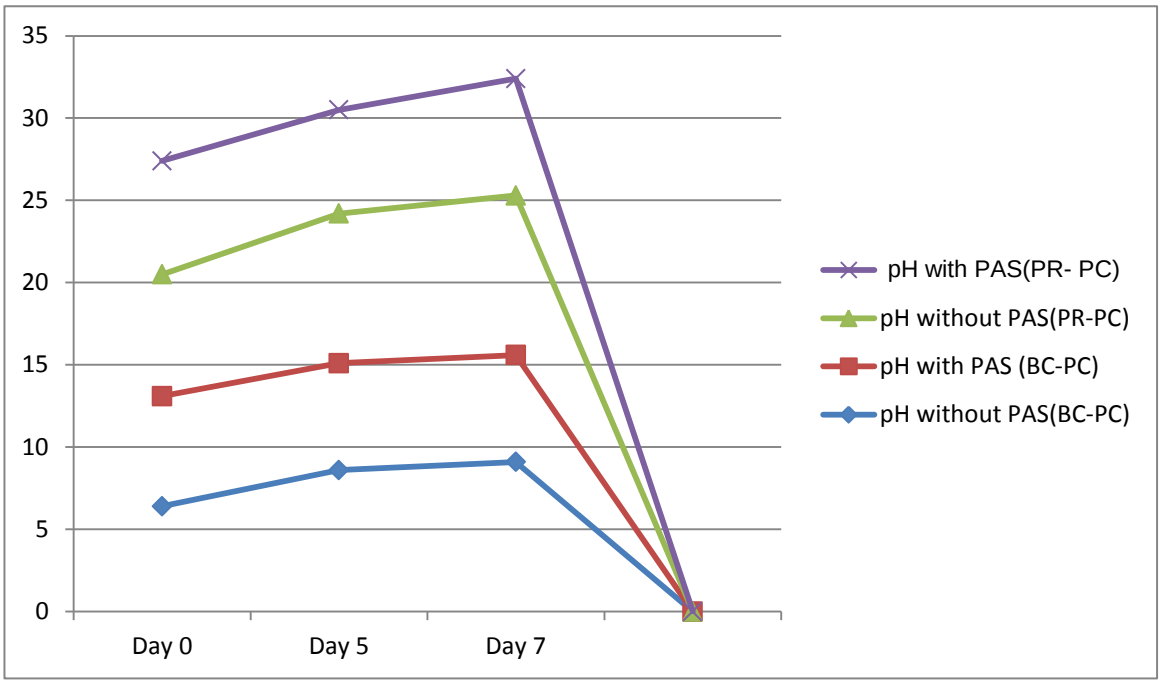


Figure 36: Comparison of pH of PCs with and without PAS for PR-PC and BC-PC respectively.

There was remarkable differences in pH between two methods from day 0 till day 7 follow up.

Grades of swirling

Table 32: Comparison of swirling of PCs with and without PAS for PR-PC and BC-PC respectively.

Storage Period	Group PR-PC (n=88)					
	Swirling without PAS (n=44)			Swirling with PAS (n=44)		
	Gr 1	Gr 2	Gr 3	Gr 1	Gr 2	Gr 3
Day 0	2	4	38	3	8	33
Day 5	5	9	30	3	4	37
Day 7	4	12	28	2	4	38
Storage Period	**Group BC-PC (n=88)**					
	Swirling without PAS (n=44)			**swirling with PAS (n=44)**		
	Gr 1	**Gr 2**	**Gr 3**	**Gr 1**	**Gr 2**	**Gr 3**
Day 0	1	3	40	4	5	35
Day 5	2	7	35	2	4	38
Day 7	6	8	30	2	2	40

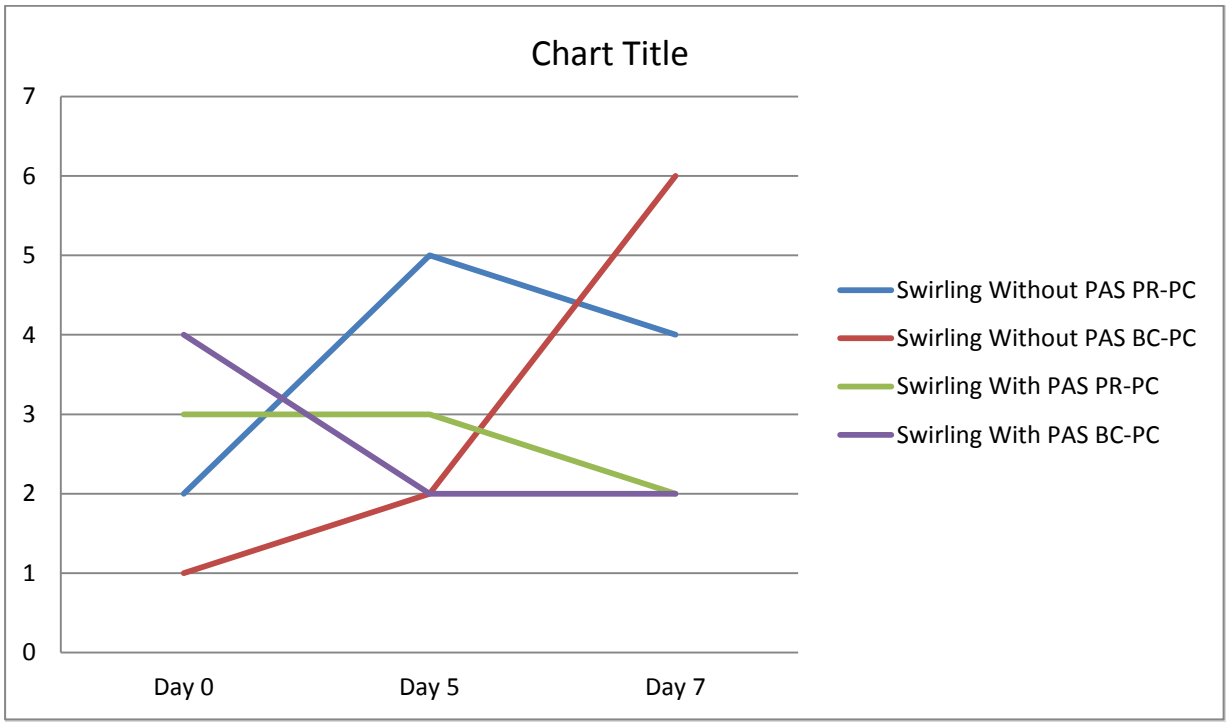


Figure 37 a: Swirling phenomena (Grade 1) noted among the PCs with and without PAS on Day 0,5 and 7

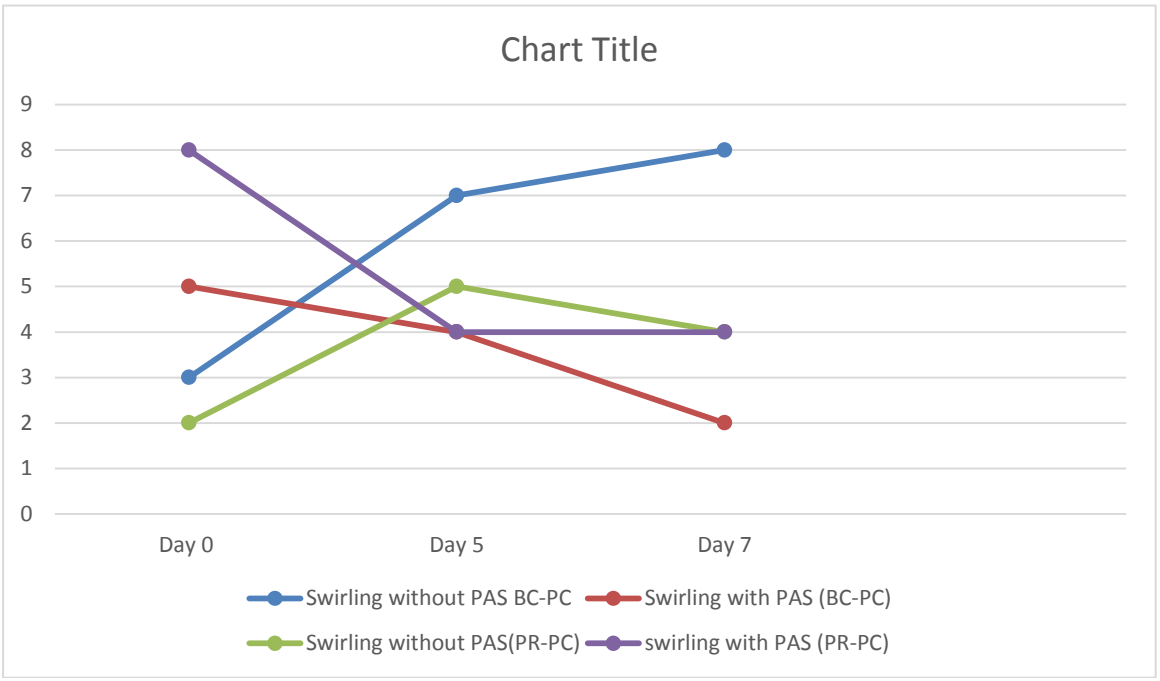


Figure 37 b: Swirling phenomena (Grade 2) noted among the PCs with and without PAS on Day 0,5 and 7

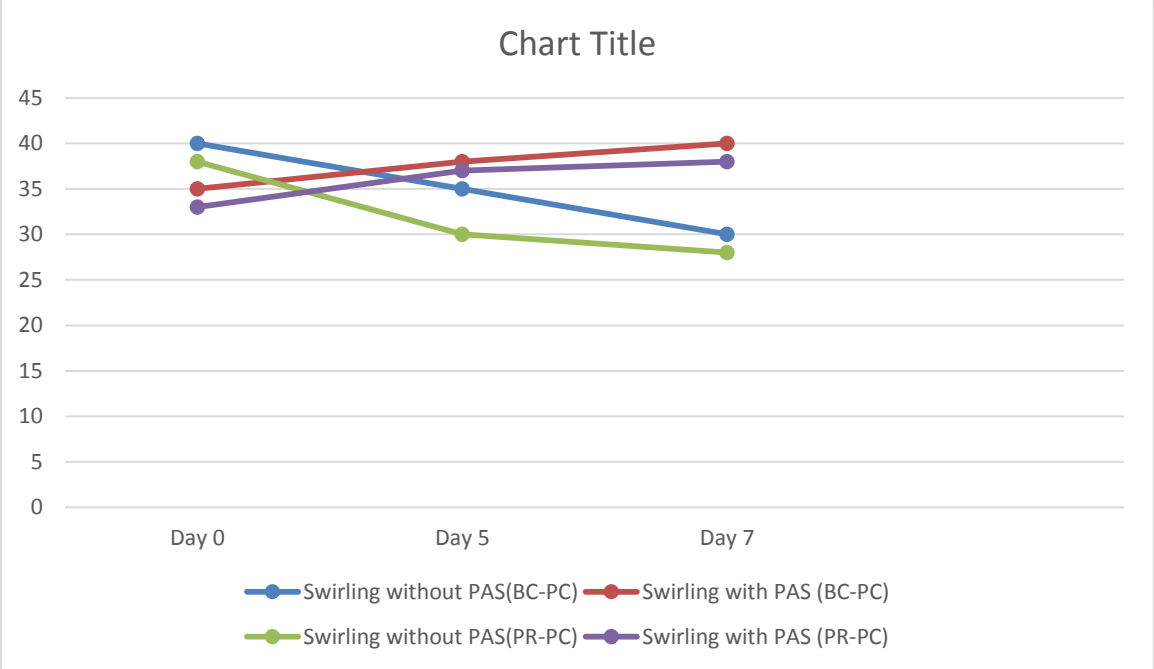


Figure 37 c: Swirling phenomena (Grade 3) noted among the PCs with and without PAS on Day 0,5 and 7.

Estimation of pCO_2

Table 33: Estimation of pCO_2 levels in PR-PC and BC-PC categories without PAS and with PAS. The pCO_2 decreased in both the categories but the decreased was more significant in PCs without PAS.

PR-PC (n=88)	**Mean**		**Std. Deviation**	**t value**
	With Out PAS (n=44)	**With PAS (n=44)**		
Day 0	126.45	123.95	6.8124	
Day 5	125.32	122.67	6.8512	-10.625
Day 7	122.85	120.88	6.8341	-13.985
BC-PC (n=88)	**Mean**		**Std. Deviation**	**t value**
	With Out PAS (n=44)	**With PAS (n=44)**		
Day 0	125.954	122.771	6.8044	
Day 5	121.265	119.556	6.8417	-10.661
Day 7	118.525	117.482	6.8296	-13.855

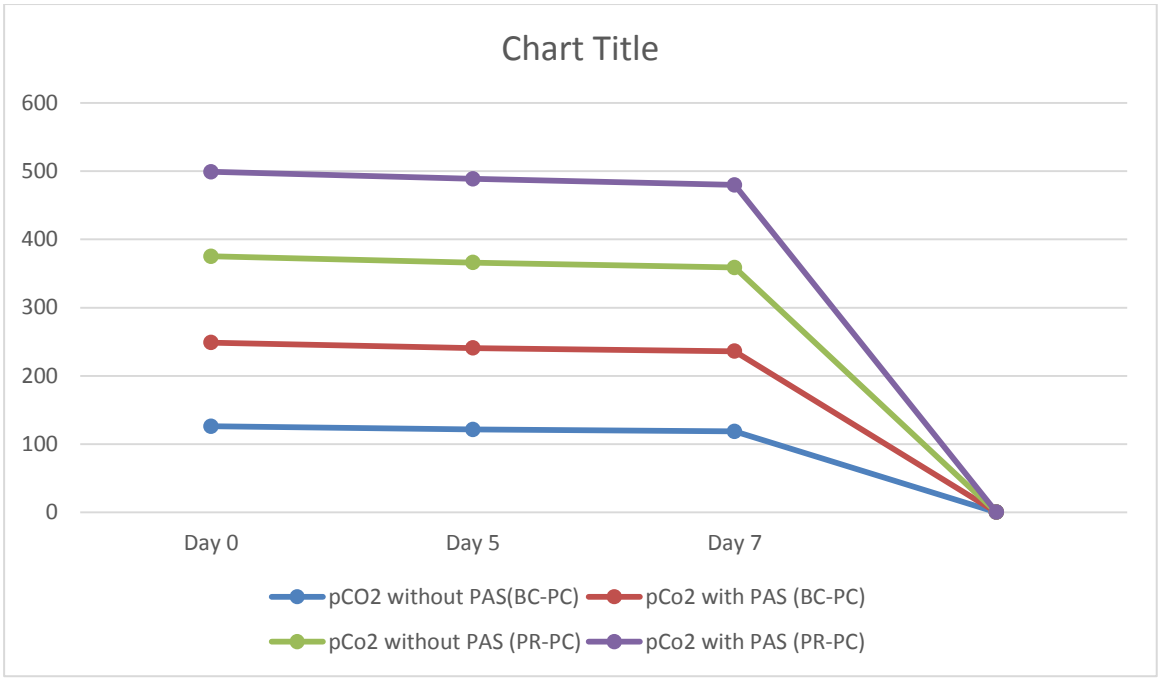


Figure 37 d: pCO2 comparison of PCs between without and with PAS across 0,5 and 7 days.

Estimation of pO2 levels

Table 34: Estimation of pO_2 levels in PR-PC and BC-PC categories without PAS and with PAS. The pO_2 increased in both the categories but the increase was more significant in PCs without PAS.

PR-PC (n=88)	**Mean**		**Std. Deviation**	**t value**	**p value**
	With Out PAS (n=44)	**With PAS (n=44)**			
Day 0	22.759	19.858	4.98		
Day 5	24.413	20.950	5.11	-48.246	
Day 7	27.651	21.980	5.25	-49.785	<0.0001**
BC-PC (n=88)	**Mean**		**Std. Deviation**	**t value**	**p value**
	With Out PAS (n=44)	**With PAS (n=44)**			
Day 0	20.958	21.978	4.77		
Day 5	26.080	22.546	4.76	-43.352	
Day 7	29.275	23.478	4.81	-47.962	<0.0001**

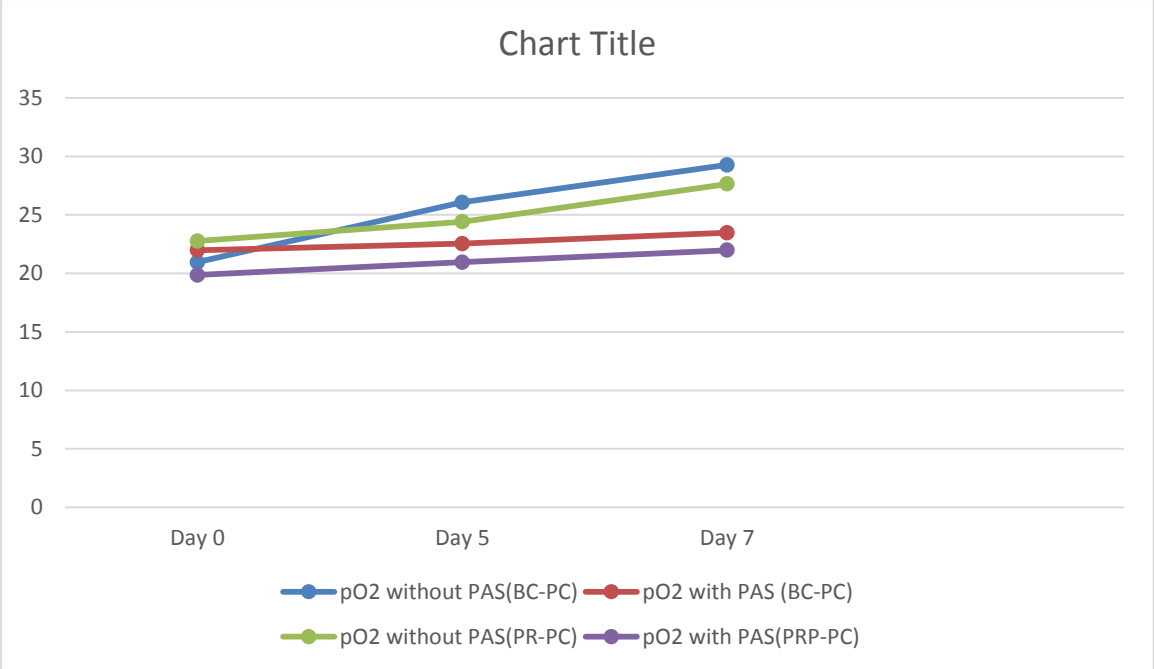


Figure 38: pO_2 comparison of PCs between without and with PAS across 0,5 and 7 days.

Estimation of Lactate Levels

Table 35: Estimation of Lactate levels in PR-PC and BC-PC categories without PAS and with PAS. Lactate levels without PAS showed progressive increase across the various days of storage whereas those with PAS had relatively lesser increase.

PR-PC (n=88)	**Mean**		**Std. Deviation**	**t value**
	With Out PAS **(n=44)**	With PAS **(n=44)**		
Day 0	312.60	290.60	2.86	
Day 5	390.53	370.60	4.02	-37.461
Day 7	401.52	392.50	3.98	-30.925

BC-PC (n=88)	**Mean**		**Std. Deviation**	**t value**
	With Out PAS **(n=44)**	With PAS **(n=44)**		
Day 0	310.62	290.32	2.53	
Day 5	340.41	307.25	3.76	-33.352
Day 7	360.95	320.47	3.71	-27.962

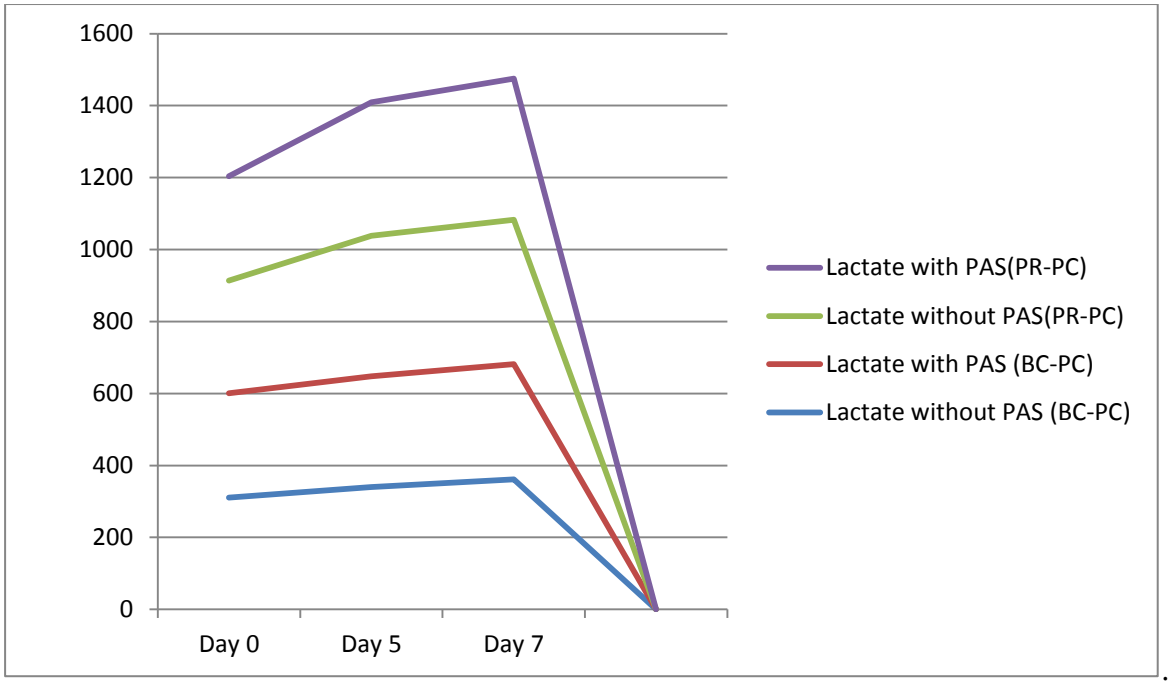


Figure 39: Lactate comparison of PCs between without and with PAS across 0,5 and 7 days.

Estimation Platelet Glucose Levels

Table 36: Estimation of glucose levels in PR-PC and BC-PC categories without PAS and with PAS. Glucose levels without PAS showed progressive decrease across the various days of storage whereas those with PAS had relatively lesser reduction.

PR-PC (n=88)	Mean		Std. Deviation	t value
	Without PAS **(n=44)**	With PAS **(n=44)**		
Day 0	410.50	401.52	3.22	
Day 5	365.21	390.53	4.28	-35.451
Day 7	295.51	312.60	4.01	-29.780
BC-PC (n=88)	Mean		Std. Deviation	t value
	Without PAS **(n=44)**	With PAS **(n=44)**		
Day 0	392.50	375.46	2.53	
Day 5	370.60	355.79	3.76	-33.352
Day 7	290.60	295.12	3.71	-27.962

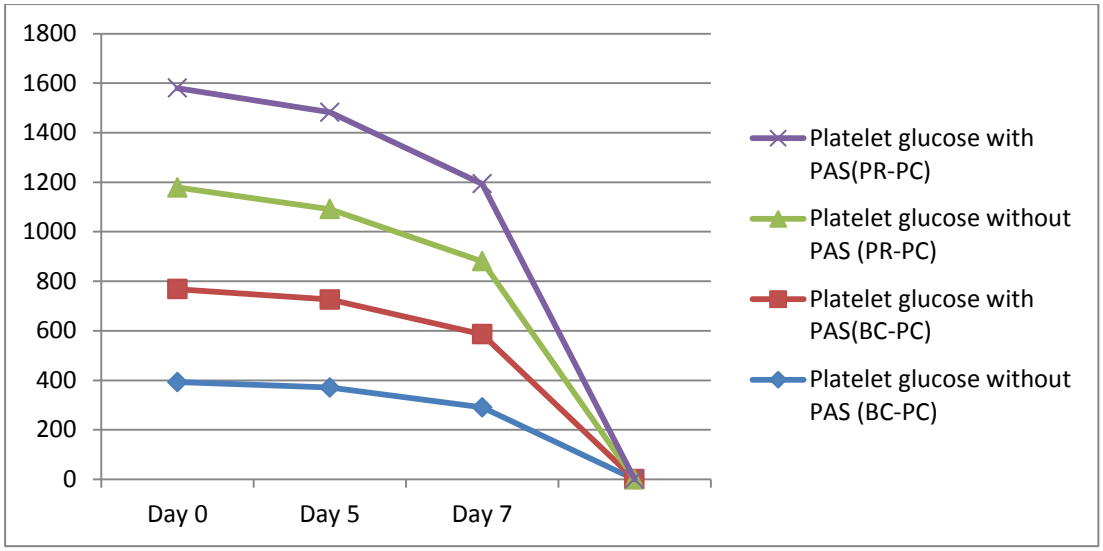


Figure 40 : Platelet glucose comparison of PCs without and with PAS across 0,5 and 7 days.

Estimation of Interleukin-1

Table 37: Interleukin -1(IL-1) In comparison between PCs without and with PAS. Significant differences were noted between different categories of PC across 0, 5 and 7 days respectively

PR-PC (n=88)		**Mean**	**Std deviation**	**t**	**df**	**Significance (2-tailed)**
Day 0	Without PAS IL **(n=44)**	82.251	52	-14.63	51	0.001
	With PAS IL **(n=44)**	78.325	52			
Day 5	Without PAS IL **(n=44)**	108.246	52	76.457	51	0.001
	With PAS IL **(n=44)**	95.236	52			
Day 7	Without PAS IL **(n=44)**	211.236	52	35.875	51	0.001
	With PAS IL **(n=44)**	182.245	52			
BC-PC (n=88)		**Mean**	**Std deviation**	**t**	**df**	**Significance (2-tailed)**
Day 0	Without PAS IL **(n=44)**	80.148	50	-12.50	49	.000
	With PAS IL **(n=44)**	75.151	50			
Day 5	Without PAS IL **(n=44)**	100.890	50	68.023	49	.000
	With PAS IL **(n=44)**	89.883	50			
Day 7	Without PAS IL **(n=44)**	117.185	50	32.471	49	.000
	With PAS IL **(n=44)**	99.623	50			

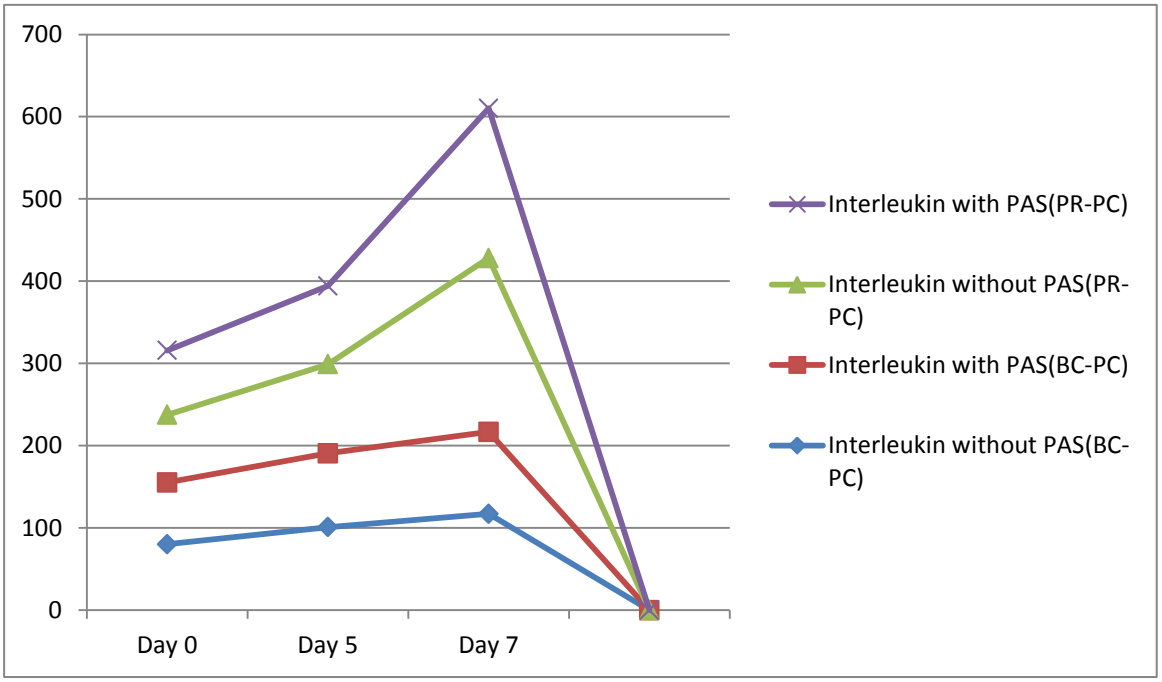


Figure 41: showing Interleukin -1(IL-1) levels between PCs without and with PAS across 0,5 and 7 days.

Estimation of TNF alpha

Table 38: Showing TNF – alpha in comparison between PCs without and with PAS.

PR-PC (n=88)		**Mean**	**Std deviation**	**t**	**df**	**Significance (2-tailed)**
Day 0	TNF –alpha(pg/ml) without PAS **(n=44)**	54	8.254	-0.144	51	0.962
	TNF –alpha(pg/ml) with PAS **(n=44)**	54.1	12.562			
Day 5	TNF –alpha(pg/ml) without PAS **(n=44)**	58.16	9.256	0.072	51	0.987
	TNF –alpha(pg/ml) with PAS **(n=44)**	57	13.256			
Day 7	TNF –alpha(pg/ml) without PAS **(n=44)**	59.25	10.205	-21.34	52	0.01
	TNF –alpha(pg/ml) with PAS**(n=44)**	60.86	11.004			
BC-PC (n=88)		**Mean**	**Std deviation**	**t**	**df**	**Significance (2-tailed)**

Day 0	TNF –alpha(pg/ml) without PAS **(n=44)**	52	7.995	-0.124	54	0.901
	TNF –alpha(pg/ml) with PAS **(n=44)**	51.7	10.479			
Day 5	TNF –alpha(pg/ml) without PAS**(n=44)**	54.22	7.769	0.041	53	0.968
	TNF –alpha(pg/ml) with PAS **(n=44)**	54	10.299			
Day 7	TNF –alpha(pg/ml) without PAS **(n=44)**	56.75	8.055	-19.243	54	0.00
	TNF –alpha(pg/ml) with PAS **(n=44)**	57.23	10.001			

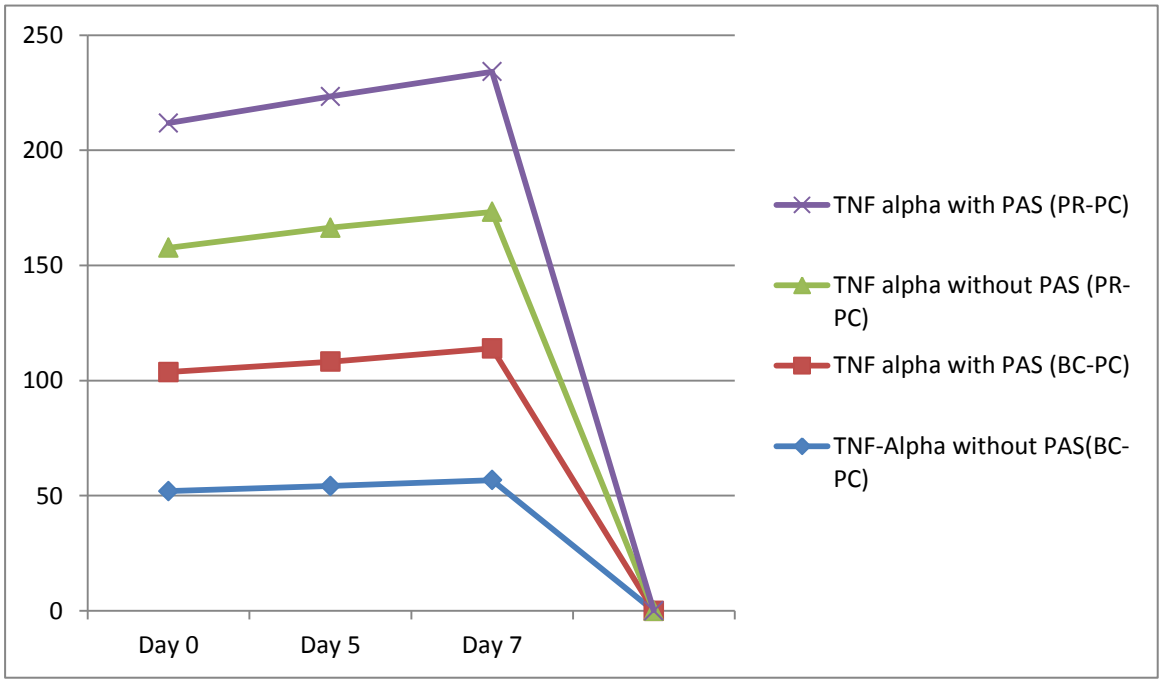


Figure 42: Showing TNF– alpha levels between PCs without and with PAS across 0,5 and 7 days.

Discussion:

The PSL results from a complex process that is influenced by physical chemical and metabolic factors related to platelet preparation and storage. Morphological alteration in platelet indices reflect the various changes associated with onset of PSL.[104] Optimized synthetic storage media might help attenuate the PSL, thereby facilitating extended storage. In an additive solution unit, the final medium contains 20-30% donor plasma.

This carry over plasma provides glucose for platelet metabolism.[105] PAS contains acetate, which serves as a second metabolic fuel. Acetate has additional benefit of acting as a buffer. PAS contains K^+ and $Mg.^{2+}$ [106] These electrolytes inhibit platelet aggregation and activation, although their mechanism work is unclear. K^+ has as an important role in maintaining the platelet membrane potential and when absent, K^+ will leak rapidly from the platelet and needs to be recovered by energy requiring K^+ pumps.[107] Presence of external magnesium activates various potassium pumps. Evidence suggests that Mg^{2+} decreases the influx of calcium and the degree of platelet activation thereby having an effect on the intracellular concentration of potassium as well.[108]

According to Gullikson et al[109] Three major points in the storage of production of PCs are essential to maintain platelet quality. First, during collection, activation of PCs should be reduced to bare minimum. Second, at the glycolytic activity level: anaerobic glucose consumption and lactate should be kept to a minimum level as well. Third, some glucose should be present in the PCs throughout the storage period. Currently, all efforts in developing new PASs are directed at producing a storage environment that allows optimization of viability, energy metabolism, and the ability of PCs to undergo hemostatic activation after transfusion.[110]

As the lactate production caused by glycolysis was supposed to be the vital cause for pH fall in stored PCs, the absolute need for glucose in a storage media was questioned. During storage at RT, PCs use the anaerobic pathway of glycolysis for energy production only to a minor extent, (approximately 15%), whereas the main part of the required energy (85%) is generated through the oxidative pathway of the TCA cycle.[111] FFAs are the major substrates representing the formerly described unidentified endogenous fuel. However need for glucose at the time of storage is reduced by acetate in PAS, but it is not efficient to maintain PC function and energy levels.[112] Furthermore, glucose complete depletion is associated with PC dysfunction as that the despite a normal pH observed by Gulliksson et al.[109] and presence of glucose is necessary in storage period for successful PC storage**.**

In order to act an effective plasma substitute, additive solution should have osmotic neutrality and with minimal energy and with minimal buffering effect. The approximate formulations of several PAS are shown in Table 24. As is evident, NaCl is common of all PAS but the molarity varies between 75 and 120mm. Glucose is present in some formulations (PAS-G, and Mg-Sol), but not in others (so called non-glucose PAS). Both types of PAS contain sodium acetate as an important ingredient [113] Sodium acetate is a two carbon molecule which can cross the mitochondrial membrane without need for transport facilitation using the carnitine system.[114] Sodium acetate is metabolized to carbon dioxide in the TCA cycle and the NADH produced generates ATP. H_2O reacts with CO_2 covalently to HCO_3^- produce adds additions buffering capacity to the milieu.[115] Glucose is an essential requirement and in the non-glucose PAS, glucose is supplied by retained anticoagulant plasma which commonly compromises ~30% of the suspending fluid. [114]

Beta-Oxidation of long –chain fatty acids such as oleic and palmitic acid is concurrent with glucose oxidation in the PCs during storage.[116] Maximizing ATP production using fatty acid oxidation would decrease the need for ATP production via glycolysis and hence decrease lactate production and the fall in pH.[117] However, the degree of benefits appears minimal and would be predicted to improve viability to any material extent [118.]Sodium citrate is common substrate for the TCA cycle and is weak buffer.[119] Sodium gluconate, and phosphate are present in some PAS. Both of these ingredients appear to retard the storage associated decline in pH, presumably acting as buffers.[120]

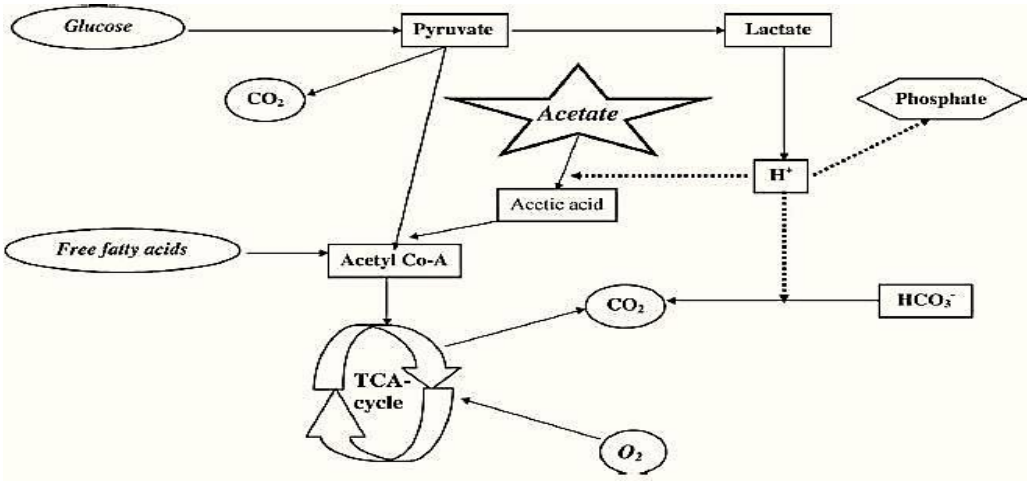


Figure 43: Metabolic pathways of PLTs with a focus on the role of acetate and the buffering of hydrogen ions derived from anaerobic glycolysis. Beside free fatty acids, acetate can serve as substrate for the oxidative metabolism in the TCA cycle. Furthermore, acetate can act as an alternate buffer to HCO_3 and phosphate (adapted from Grey D et al. 2015-75:110-4).[121]

PAS contains K^+ and Mg^{2+} are present in some but not others. Mg^{2+} is considered to reduce platelet activation in vitro and both K^+ and Mg^{2+} decrease glucose consumption.[122] These ingredients are not present in PAS III or Intersol.[122] Despite these manipulations of the clinical studies to measure efficacy as measured by platelet count increment in thrombocytopenic recipients have shown mixed results with some showing inferiority to plasma storage. However, Saunders C et al[123] have conducted studies with non-glucose containing PAS showing improved increments.[123]

Several studies conducted by Snyder et al,[124] Metcalfe et al [125] and Shanwell et al [126] prove that onset of PSL is dependent on cytokine generation and release including the levels of RANTES, beta- thrombo globulin, PF-4, IL -7 were markedly increased in PRP- PC samples as compared to BC-PC samples. The present study has reinforced the fact that the presence of Mg^{2+} helps in minimizing cytokine generation and release in the stored PCs. However, Costa et al [127] undertook the serial estimation of IL-1, IL-6, IL-7, TNF-alpha and CD-62 (P-selectin) and observed no significant variation between stored PRP-PC versus BC-PC samples. Hence more studies are needed to reach to a conclusive opinion.

Current study demonstrated that PAS is effective in significantly lowering the generation and release of cytokines whereas the IL level showed only minor variation during the entire storage period and the TNF-alpha showed no significant increase during the storage period. Identical findings were also noted in recent studies conducted in Europe by Tynngard et al.[128] This study reveals the role of cytokines towards progression of PSL and also show the advantages of having PAS in routine usage. Hence, efforts must be made to minimize "contact activation" of PCs during routine preparation and storage.

Conclusion:

Current study states that the viability of PCs are maintained for additional 3 days (i.e. upto 7 days) without compromising their functional abilities. Hence the shelf life of PCs can be extended for more than 5 days. However, further studies are required to correctly assess the *in- vivo* qualities of stored PCs in PAS.

CHAPTER V

FLOW CYTOMETRY ASSAY OF CD62 AND ANNEXIN V IN STORED PLATELETS WITH AND WITHOUT PAS

Introduction

FC is the technique for cell counting and measurement of different properties of all cell ('cyto'= Cell; 'metry'= count/measurement). It is a laser based technology that measures and analyses different physical and chemical properties of the cells/particles flowing in a stream of fluid through a beam of light. An optical-to-electronic coupling system is used to record the way in which the particle emits fluorescence and scatters incident light from the laser.[129]

For the platelet function analysis, FC has emerged as a very useful tool. Platelet activation is associated with surface expression of proteins not found on quiescent PCs. Analysis of these proteins has been used to evaluate in vivo platelet activation, which occurs in various clinical settings.[130]

The principle is intensity of the emitted light is directly proportional to the number of antibodies attached to the platelet receptors/antigens which get attached upon activation. CD62P is a membrane glycoprotein in alpha-granules of PCs. On activation of PCs, exocytosis of the alpha-granules leads to CD62P exposure on the platelet surface. CD62P expression reflects the degranulation of PCs and thus serves as a moderately sensitive marker for the activation status of PCs in vitro and in vivo. Annexin V is very often used to detect apoptotic cells by its ability to bind to phosphatidylserine is expressed during apoptosis.[131]

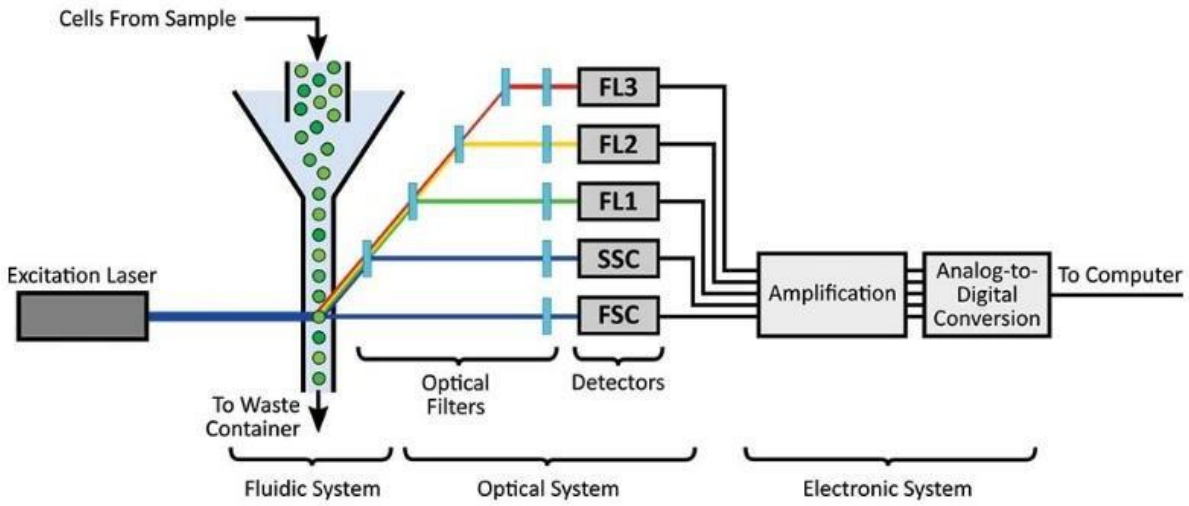


Figure 44(a): Principles of Flow Cytometry (adapted from Paulus JM 1975;46:321–36)[12]

Aim and Objectives –

1. To analyze the level of expression of activation markers (CD62 and Annexin V) among WB derived PRPC and BC-PC along with the respective platelet sub population suspended in plasma beyond 5 days.
2. To analyze the level of expression of activation markers (CD62 and Annexin V) among WB derived PRPC and BC-PC along with the respective platelet sub population suspended in PAS beyond 5 days.

Materials and Methods –

Principle: FC is based on hydrodynamic focusing where single cells pass the detection point, where a laser beam is focused by lenses to a narrow area ensuring single cell illumination. Light reflected by the cell will be scattered in different directions. In addition to the scattered light, fluorescence can also be measured. FC consist of a fluidic system where cell movement occurs in a laminar flow, thus cell passage occurs in a single file.[132]

Forward scatter: The forward scatter corresponds roughly to the size of the cell. The light may be focused to the detector using collection lenses. The light is filtered before detection.[133]

Side scatter: Side scatter corresponds more or less to the granularity of the cell. Side scatter is collected perpendicular to the laser beam, and may be focused using collection lenses.[133]

Fluorescence: A FC can have several lasers and detectors to allow information on a number of different fluorophores. Light of different wavelengths are directed towards the different detectors using a set of dichroic mirrors. The dichroic mirrors reflects light of a certain wavelength while allowing other wavelengths to pass through. The fluorescence signal confers information on the abundance of a fluorophore.[133]

Detection: Stronger light signals from forward scatter (and sometimes side scatter) are detected using photodiodes, whereas the weaker fluorescent signals are detected using photomultiplier tubes. Light reaching the detectors is converted into a digital signal proportional to the light intensity of the cell.[133]

WB derived PR-PC and BC-PC were prepared as per SOP.[2] Samples were further segregated into two groups having plasma and PAS respectively under sterile conditions as already explained.[2]

A 2ml of PCs including PR-PC and BC-PC were collected separately by spiking on day 5, day 7. Similar technique was also used for Annexin V estimation. The bag was stored on platelet agitator in the intervening period. The PCs were fixed using 1% paraformaldehyde.[132]

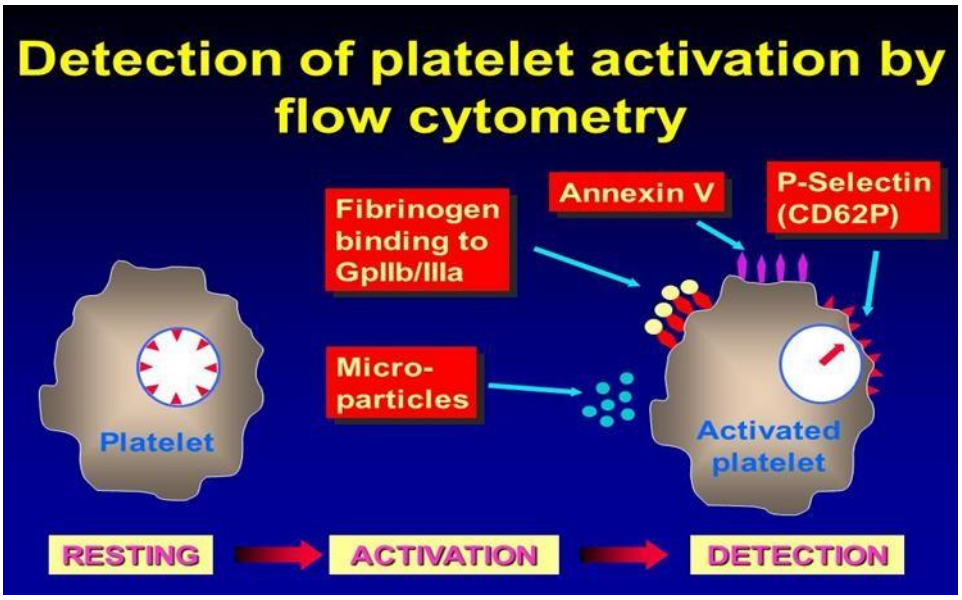


Figure 44(b); showing detection of platelet activation by flow cytometry. **(**adapted from Paulus JM et al. 1975;46:321–36)[12]

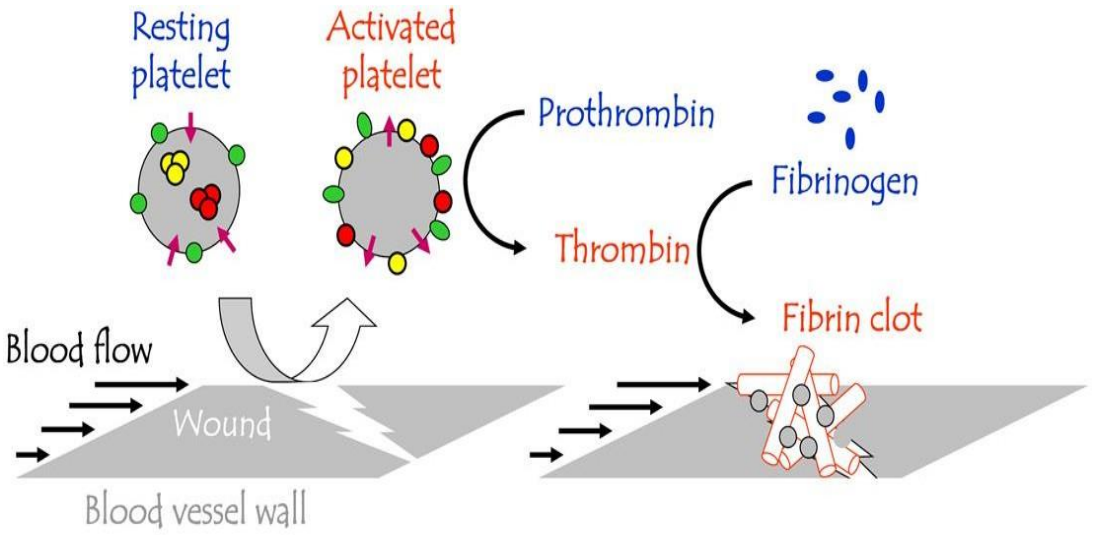


Figure 44 (c): Showing mechanism of activation of resting platelet. (adapted from Farre AL et al. 2014;18:27-36)[17]

A titration study was conducted for CD62 and annexin V using four different concentrations (1:50, 1:100, 1:200, and 1:300) to determine the optimal dilution. Before staining the cells, serial dilutions of the PCs were made with 0.9% NaCl to attain of 5×10^6 cells/mL in 5-mL

round-bottom polystyrene tubes for FC (Falcon™, Thermo Fisher Scientific, Whitby, ON, Canada**)**.[134]

The FC was subjected to the routine daily setup procedures, verification of its optical alignment together with fluidic stability (with FLOW-CHECK™ 770 fluorospheres) and standardisation of detector functions (with FLOWSET™ 770 fluorospheres), as contained in the setup kit (PC7 setup kit, Beckman Coulter; Coulter Corporation). Instrument linearity was checked with an Immuno-Brite™ Standards kit (Beckman Coulter). Colour compensation was verified with the QuickCOMP kit (Beckman Coulter).

Platelets were identified according to their forward scatter (FSC) and side scatter (SSC) characteristics and for every sample an electronic gate was drawn around total platelets along with the respective large, medium-sized and small platelet populations. The results were shown as FSC/log SSC histograms and fluorescence intensity/cell count histograms.[135]

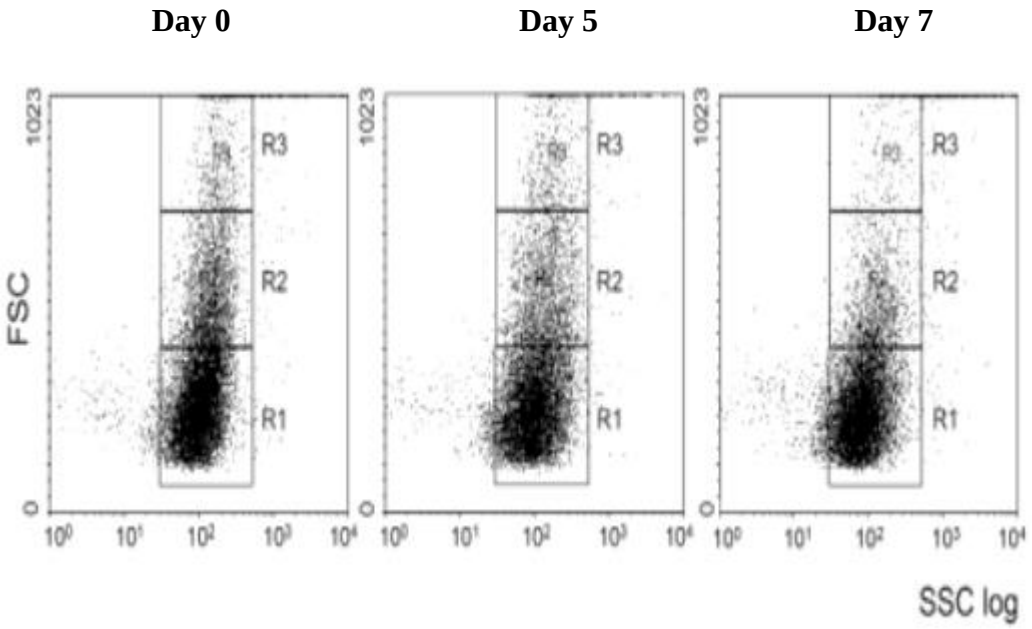


Figure 45: Distribution of platelet subpopulation with large, medium and small volume based on FSC/log SSC values.

The 3 sub categories of platelets, namely, large, medium and small were gated to distinguish the different subpopulation accordingly. Binding of antibodies and probes to platelets was determined as median fluorescence intensity (MFI) or as percentage positive platelets.[136] The boundary between positive and negative platelets was set using a negative control/isotype control sample, where a gate was placed to give 1–2% positive platelets in a fluorescence histogram including all platelets as per manufacturers protocol.[136] The statistical significance

of differences between two groups was determined by the paired two-tailed Student's t-test. Individual platelets were analyzed and to eliminate the risk of bias the respective gates were not further adjusted during the course of platelet activation markers.A minimum 5000-6000 events were noted.[136]

CD-62

The CD62P expression on the platelet surface was determined by FC using 1 mL of PC sample.[137] PC samples were diluted 1:100 (to approximately 1.107/mL) using a diluent consisting of the same PAS used for PC production (either PAS-B or PASE; SSP or SSP+ [Macopharma, Tourcoing, France]) with 0.5% w/v bovine serum albumin (Sigma-Aldrich, St. Louis, MO, USA). Fifty microliters of diluted PC sample were labeled using 2 µL of fluorescein isothiocyanate (FITC)-coupled anti-CD41 (FITC mouse antihuman CD41, clone HIP8 [Becton Dickinson, Franklin Lakes, NJ, USA]) and 5 µL of phycoerythrin-cyanine 5 (PE-Cy5)-coupled anti-CD62P (PE-Cy5 mouse anti-human CD62P, clone AK-4 [Becton Dickinson]).

For each sample an isotype control sample (50 µL of diluted PC sample labeled with 5 µL of PE-Cy5 mouse IgG1 κ isotype control, clone MOPC-21 [Becton Dickinson]) and a thrombin-activated positive control sample with maximum CD62P expression (50 µL of diluted PC sample labeled with 5 µL of CD62P-PE-Cy5 and activated with 1 IU/mL thrombin [Roche, Basel, Switzerland]) were prepared. Samples and controls were labeled and analyzed in BD TruCount tubes (Becton Dickinson) containing a known number of fluorescent beads. Samples were analyzed in singlicates. After labeling samples were mixed, incubated for 20 min at RT in the dark, further diluted with 500 µL of diluent, and stored in the dark until analysis.

The gated platelet population was used to calculate the percentage of CD62P-positive platelets, defined as:

• Based on the isotype control, a threshold was set to include 1% of all events with the highest fluorescence and all events with fluorescence above this threshold were defined as CD62P-positive in comparison to the isotype control.

• Based on the positive control, a threshold was defined to include 95% of the thrombin-activated platelet population with the highest fluorescence. All platelets with fluorescence above this threshold were considered CD62P-positive in comparison to the positive control.

Platelet activation state was expressed in relation to both isotype and positive control as percentage of gated platelet population above the respective CD62P positivity threshold.

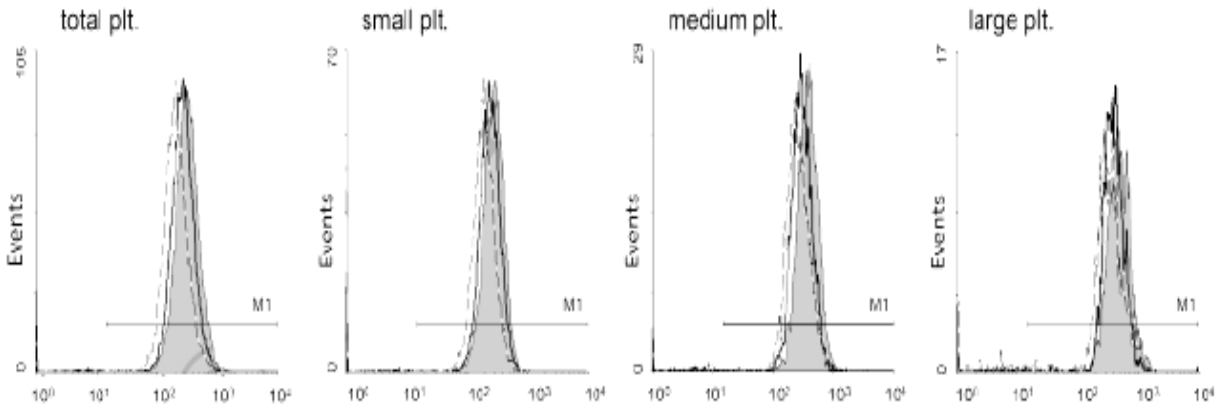


Figure 46: Total platelets and subpopulations of platelets were identified as small, medium and large based on FSC/log, SSC values

Annexin V: One milliliter of sample with 5×10^6 cells was poured into a 5-mL round-bottom polystyrene tube for FC (Falcon™, Thermo Fisher Scientific, Whitby, ON, Canada).[138] Two times the cells were washed with a phosphate-buffered saline solution, followed by centrifugation (Sorvall™ ST16 Centrifuge, Thermo Fisher Scientific, Waltham, Massachusetts, USA) at 300 g for 8 minutes. After discarding the supernatant, PCs were reconstituted with 1 mL of binding buffer (Annexin V Binding Buffer, 10X concentrate, BD Pharmingen™ Becton, Dickinson and Company, NJ, USA) and gently mixed. Subsequently, 100 µL was transferred to a 5-mL culture tube, stained with 1 µL of annexin V (FITC Annexin V Apoptosis Detection Kit I, BD Pharmingen™ Becton, Dickinson and Company, NJ, USA), and gently mixed (Vortex Genie 2, Thermo Fisher Scientific, Whitby, ON, Canada).[138] at RT for a duration of 15 minutes. All the samples were protected from light at all times.

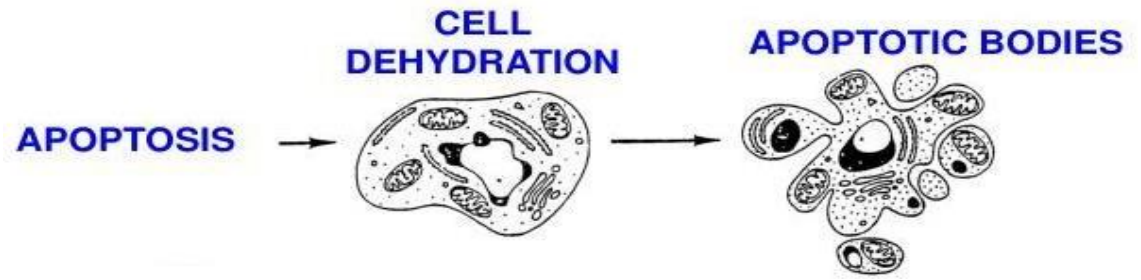


Figure 47: Showing mechanism of apoptosis. (adapted from Cognasse F et al. 2009;49:91–98).[25]

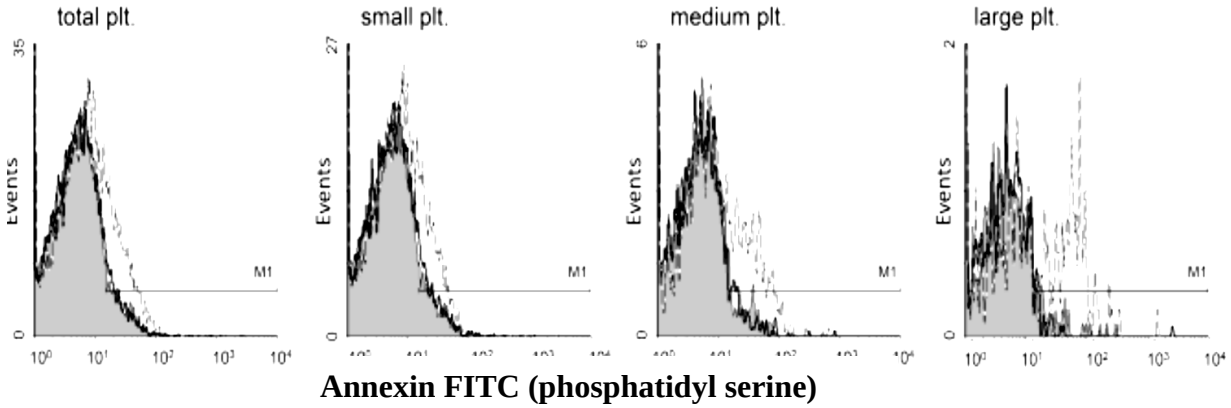


Figure 48: Total platelets and subpopulations of platelets were identified as small, medium and large based on FSC/log, SSC values

Table 39(a): Expression of CD62 and Annexin V(Phosphatidylserine) on BC-PC with PAS during various storage period along with Mean fluorescence intensity. Statistically significant difference ($p<0.05$) between: * the 0 and 5 days,† the 0 and 7 th days, and ‡ the 5 and 7th days.

Marker	Day	Positive platelets (%)			Mean fluorescence intensity		
		Small	Medium	Large	Small	Medium	Large
CD62	0	8±2	9 ±1	11±3	2.5±0.4	3.6±0.6	5.4±3.1
	5	9±3	9 ±3	8±2 *	2.9±0.4	4.2±1.7	5.6±2.8
	7	18±6 †,‡	20±8 †,‡	25±10 †,‡	2.5±0.3 ‡	3.5±0.6	6.0±4.5
Marker	**Day**	**Positive platelets (%)**			**Mean fluorescence intensity**		
		Small	**Medium**	**Large**	**Small**	**Medium**	**Large**
Phosphatidylserine (Annexin V)	0	7.3±3.5	2.2±0.8	1.6±1.1	66±25	56±24	52±22
	5	9.8±5.4	3.9±2.2	4.5±3.8	48±21	46±15	46±18
	7	8.7±4.7	3.0±1.6	2.6±2.0	42±21	50±20	76±29

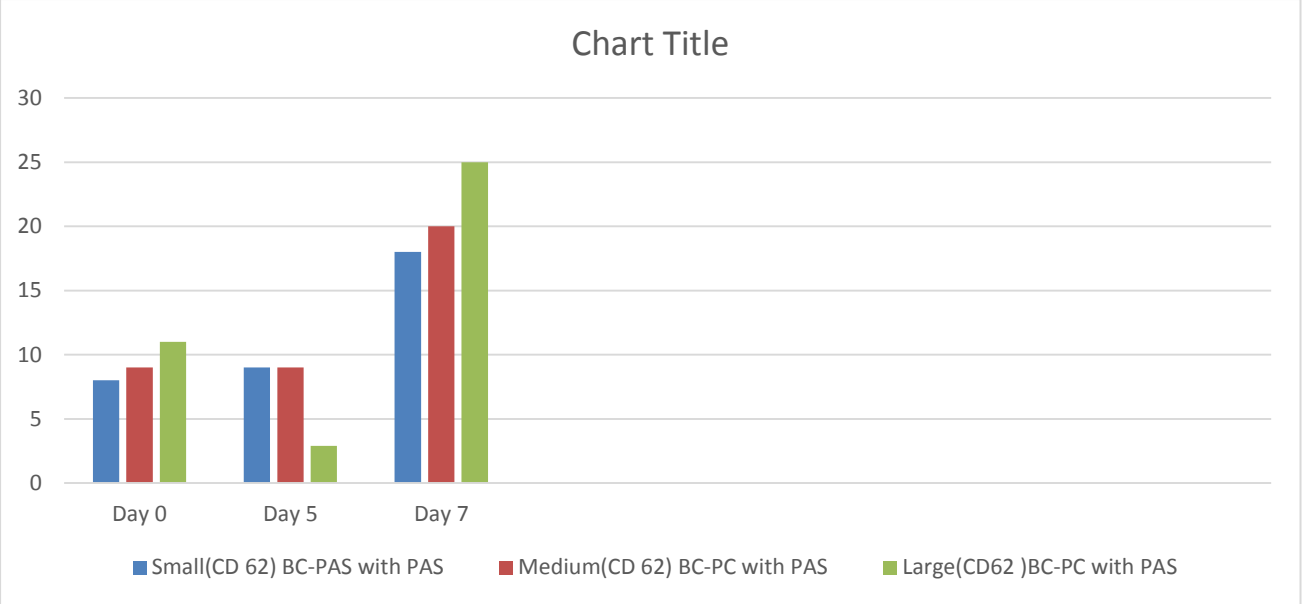


Figure 49 (a): Expression of CD62 on BC-PC with PAS during various storage period

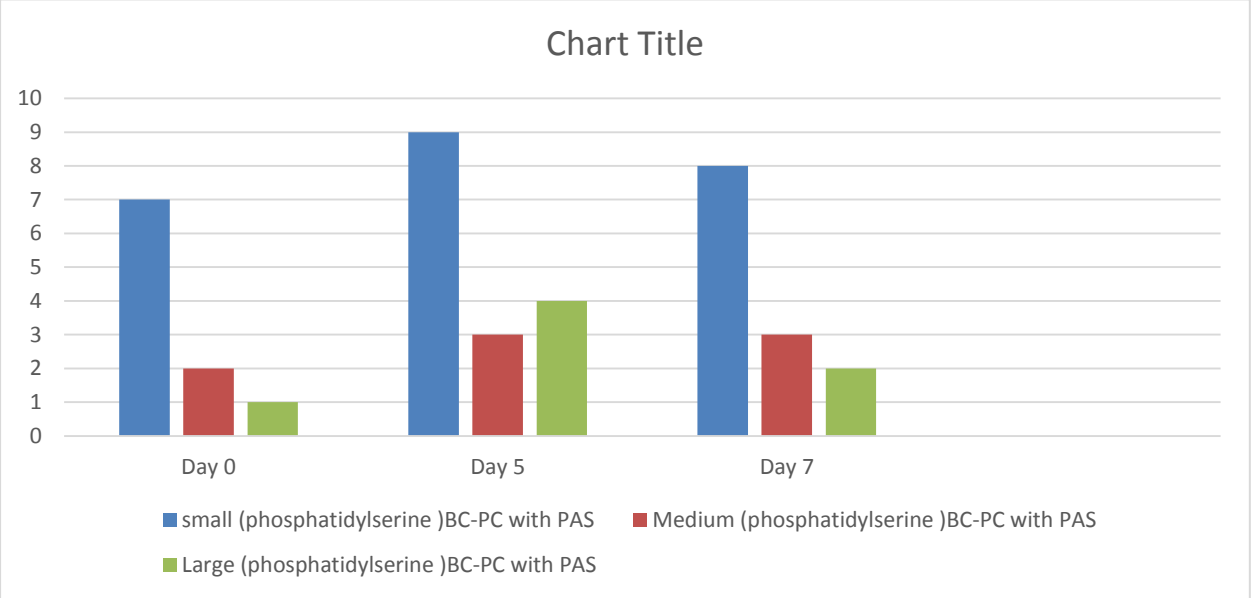


Figure 49 (b): Expression of Annexin V(phosphatidylserine) on BC-PC with PAS during various storage period

Table 39(b): Expression of CD62 and Annexin V (Phosphatidylserine) on BC-PC without PAS during various storage period along with Mean fluorescence intensity. Statistically significant difference ($p<0.05$) between: * the 0 and 5 days,† the 0 and 7 th days, and ‡ the 5 and 7th days.

Marker	Day	Positive platelets (%)			Mean fluorescence intensity		
		Small	Medium	Large	Small	Medium	Large
CD62	0	6.5±2	7.5 ±1	9.5±3	1±0.4	2.1±0.6	3.4±3.1
	5	7.5±3	7.5 ±3*	6.5±2	1.4±0.4	3.2±1.7	4.6±2.8
	7	16.5±6†,‡	18.5±8†,‡	23.5±10†,‡	0.7±0.3	2.3±0.6‡	4.8±4.5
Marker	**Day**	**Positive platelets (%)**			**Mean fluorescence intensity**		
		Small	**Medium**	**Large**	**Small**	**Medium**	**Large**
Phosphatidylserine (Annexin V)	0	5.3±3.5	0.8±0.8	0.8±1.1	64.5±25	54.5±24	50.5±22
	5	7.8±5.4	1.9±2.2	2.8±3.8	44.5±21	44.5±15	46.5±18
	7	7.2±4.7	1.8±1.6	1.8±2.0	40.5±21	48.5±20	74.5±29

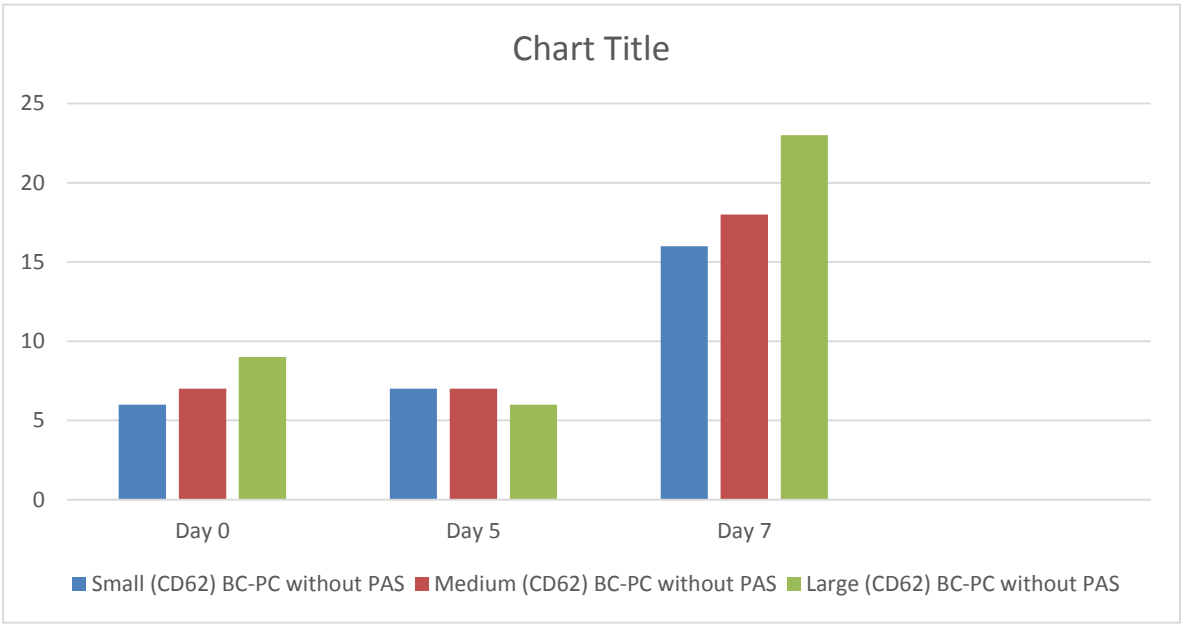


Figure 49 (c): Expression of CD62 on BC-PC without PAS during various storage period.

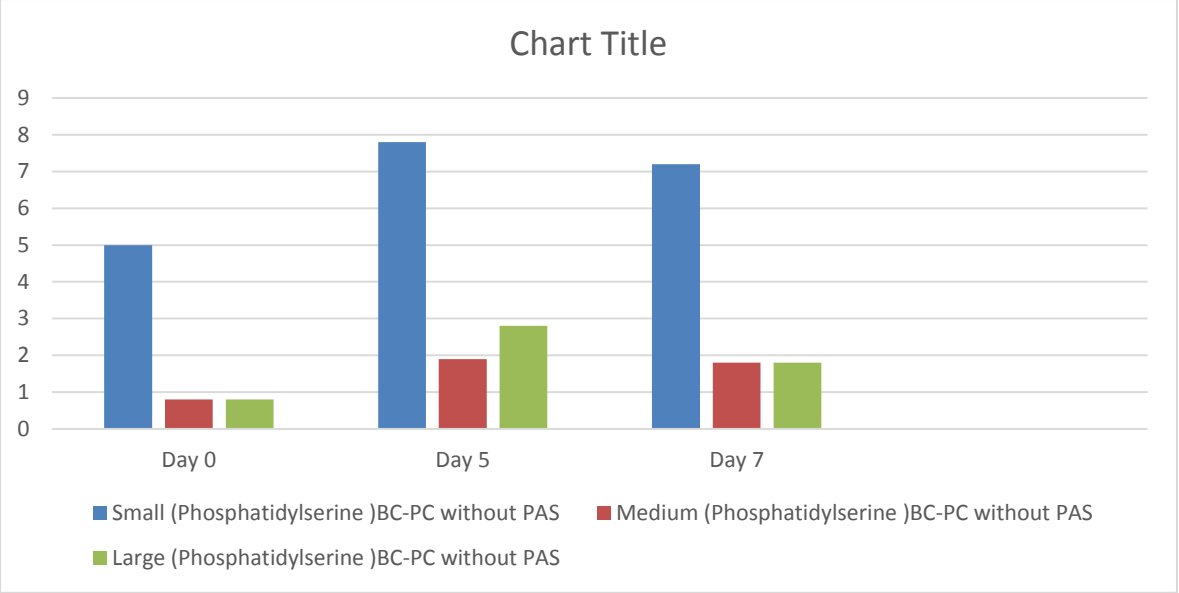


Figure 49 (d): Expression of Annexin V (Phosphatidylserine) on BC without PAS during various storage period.

Table 40(a): Expression of CD62 and Annexin V (Phosphatidylserine) on PR-PC with PAS during various storage period along with Mean fluorescence intensity. Statistically significant difference ($p<0.05$) between: * the 0 and 5 days,† the 0 and 7 th days, and ‡ the 5 and 7th days.

Marker	**Day**	**Positive platelets (%)**			**Mean fluorescence intensity**		
		Small	**Medium**	**Large**	**Small**	**Medium**	**Large**
CD62	0	9.5±2	10.5 ±1	12.5±3	4±0.4	3.6±0.6	6.9±3.1
	5	10.5±3	10.5±3	9.5±2*	4.4±0.4	4.2±1.7	7.1±2.8
	7	19.5±6†,‡	21.5±8†,‡	26.5±10†,‡	4±0.3	3.5±0.6	7.5±4.5‡
Marker	**Day**	**Positive platelets (%)**			**Mean fluorescence intensity**		
		Small	**Medium**	**Large**	**Small**	**Medium**	**Large**
Phosphatidylserine (Annexin V)	0	8.5±3.5	4.2±0.8	2.5±1.1	68±25	58±24	54±22
	5	10.2±5.4	6.5±2.2	6.5±3.8	50±21	48±15	48±18
	7	9.6±4.7	3.2±1.6	3.2±2.0	44±21	52±20	78±29

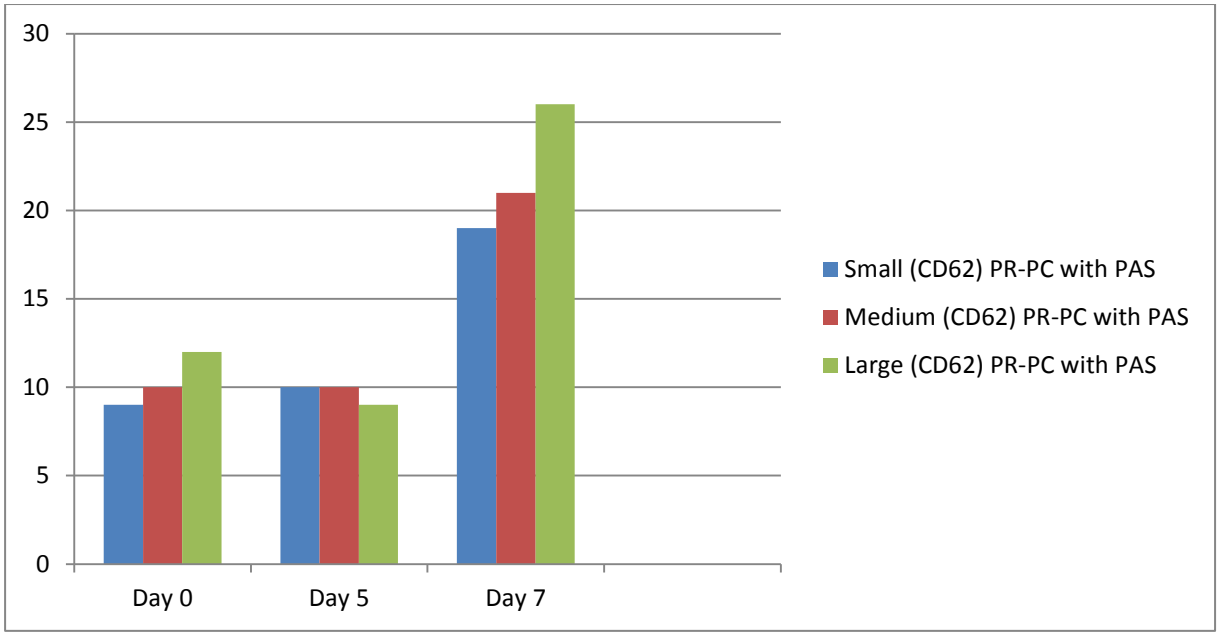


Figure 49 (e): Expression of CD62 on PR-PC with PAS during various storage period

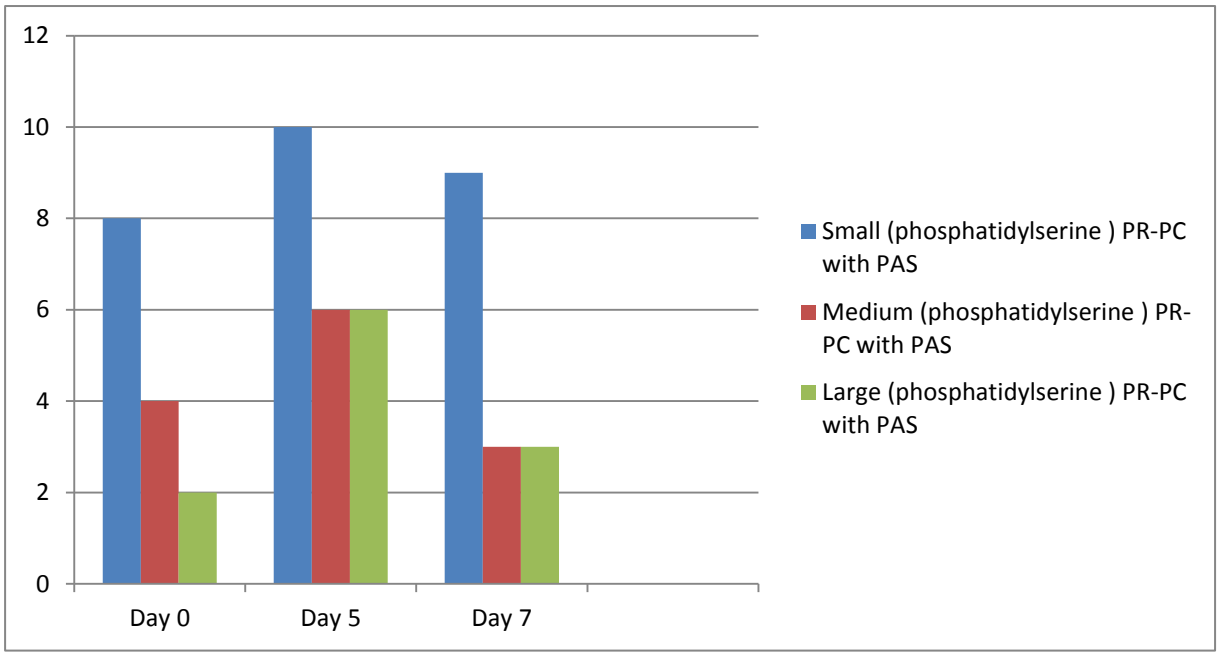


Figure 49 (f): Expression of Annexin V (Phoshpatidylserineon) PR-PC with PAS during various storage period

Table 40(b): Expression of CD62 and Annexin V (Phosphatidylserine) on PR-PC without PAS during various storage period along with Mean fluorescence intensity. Statistically significant difference ($p<0.05$) between: * the 0 and 5 days,† the 0 and 7 th days, and ‡ the 5 and 7th days.

Marker	Day	Positive platelets (%)			Mean fluorescence intensity		
		Small	Medium	Large	Small	Medium	Large
CD62	0	10.5±2	12 ±1	14±3	5.5±0.4	5.1±0.6	7.4±3.1
	5	12±3	12±3	11±2*	5.9±0.4	5.6±1.7	8.6±2.8
	7	21±6†,‡	23±8†,‡	28±10†,‡	5.5±0.3‡	5±0.6	9±4.5
Marker	**Day**	**Positive platelets (%)**			**Mean fluorescence intensity**		
		Small	**Medium**	**Large**	**Small**	**Medium**	**Large**
Phosphatidylserine (Annexin V)	0	9.5±3.5	5.2±0.8	3.5±1.1	66.5±25	56.5±24	52.5±22
	5	11.2±5.4	7.5±2.2	7.5±3.8	48.5±21	46.5±15	46.5±18
	7	10.2±4.7	4.2±1.6	4.2±2.0	42.5±21	50.5±20	76.5±29

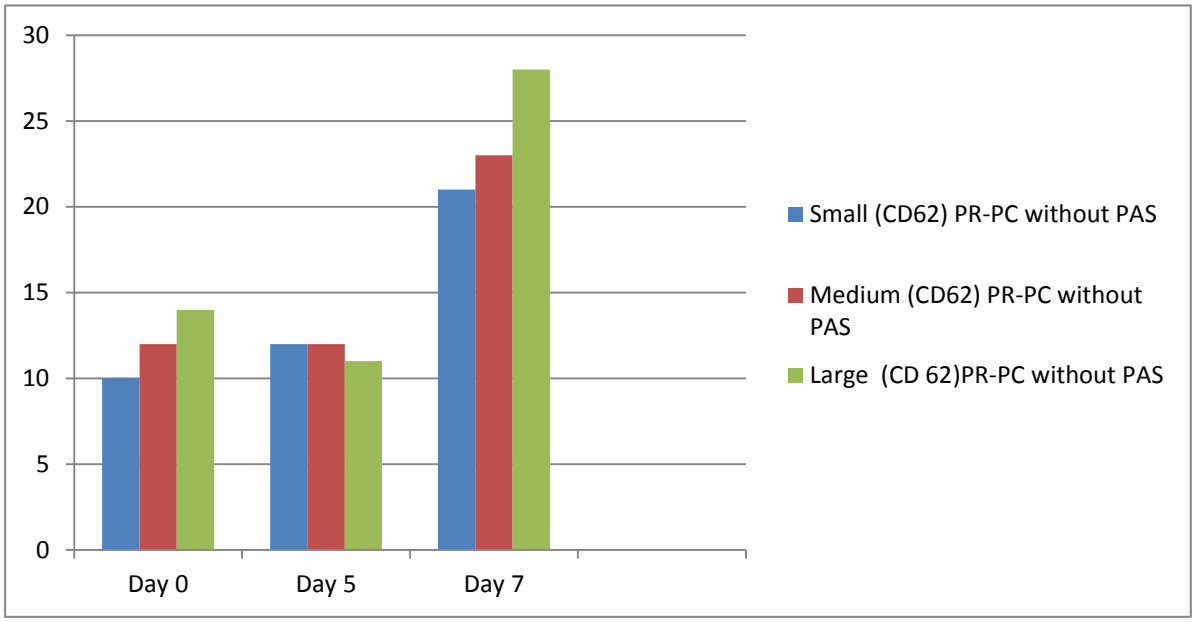


Figure 49 (g): Expression of CD62 on PR-PC without PAS during various storage period.

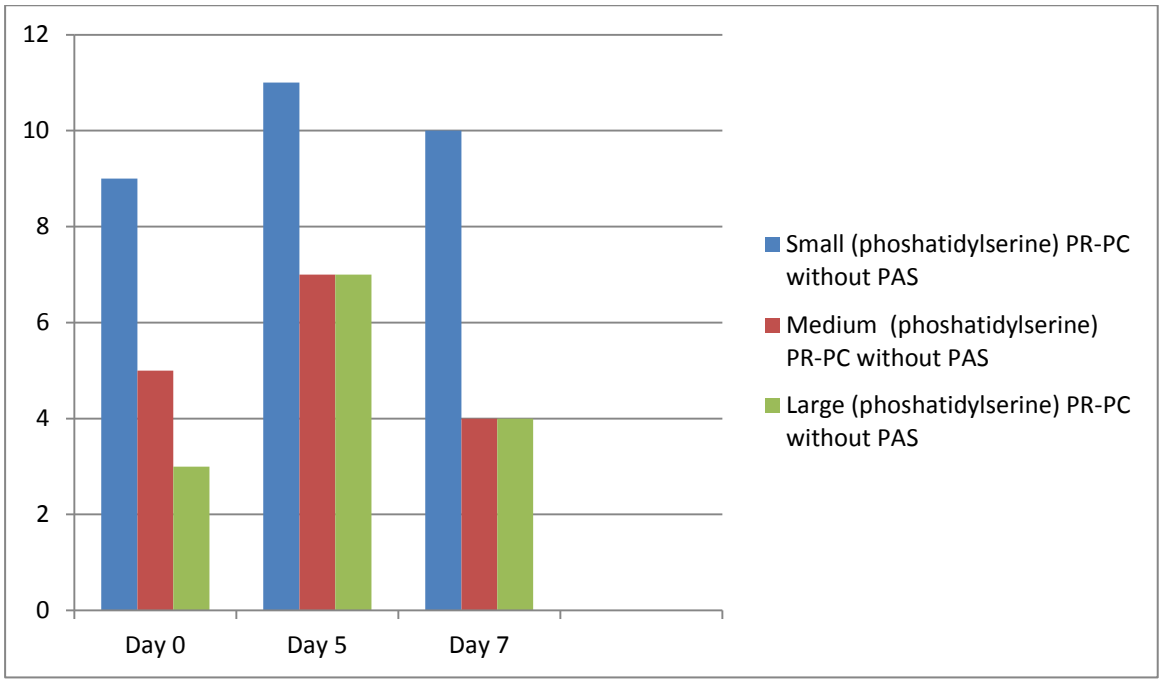
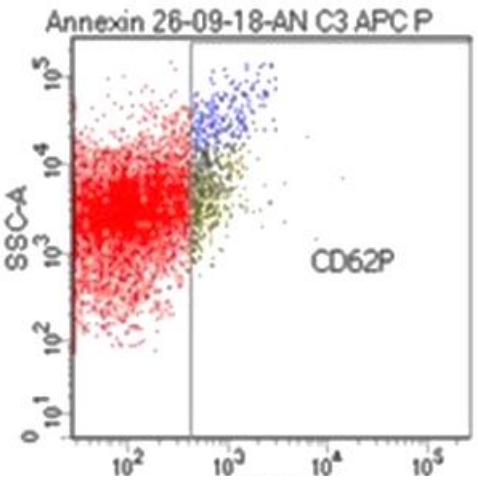
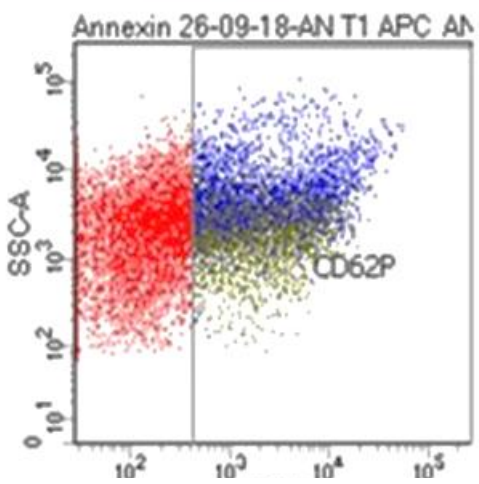


Figure 49 (h): Expression of Annexin V (Phopshatidylserine) on PR-PC without PAS during various storage period





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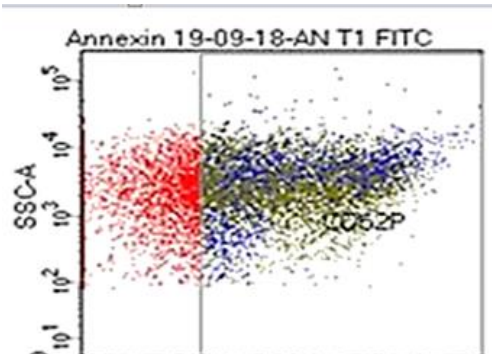

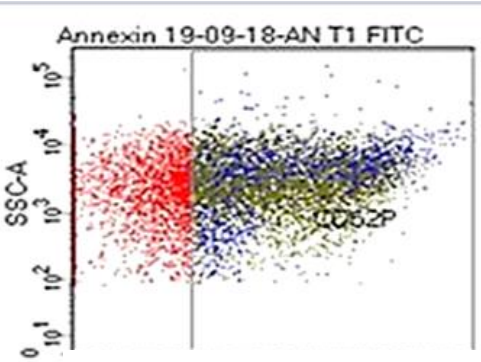

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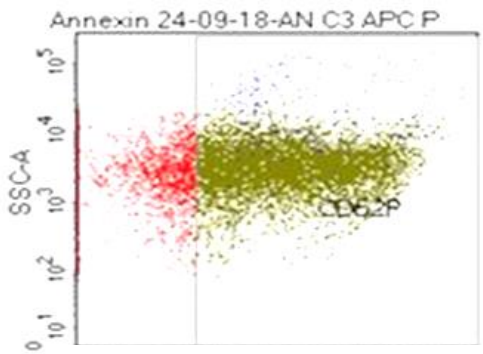

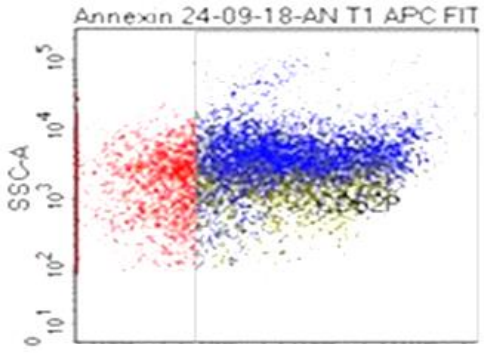

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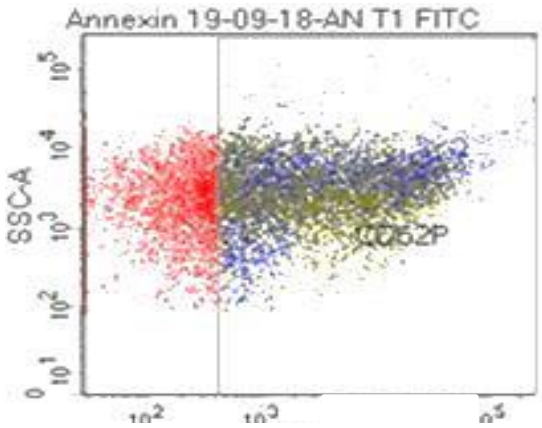
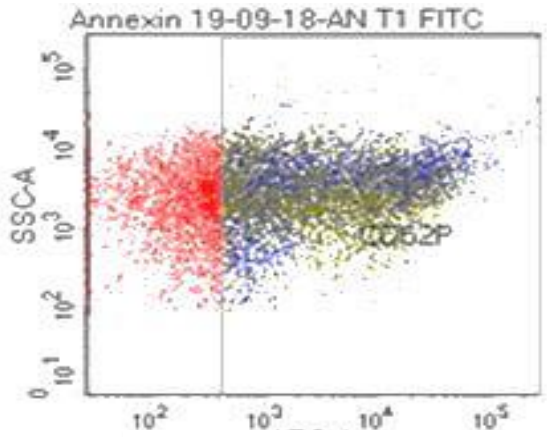
Figure 50 (a): MFI for CD62P and Annexin V(phosphatidylserine) **PR-PC with PAS** on day 7(maximum day of storage)





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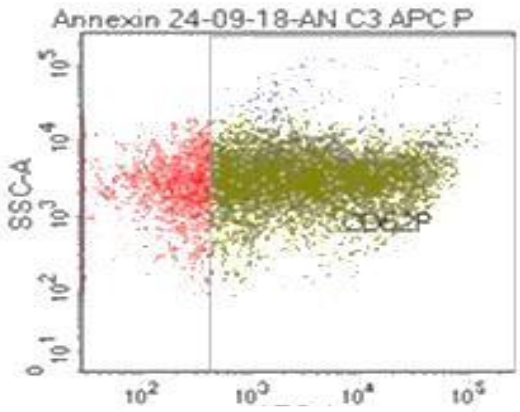

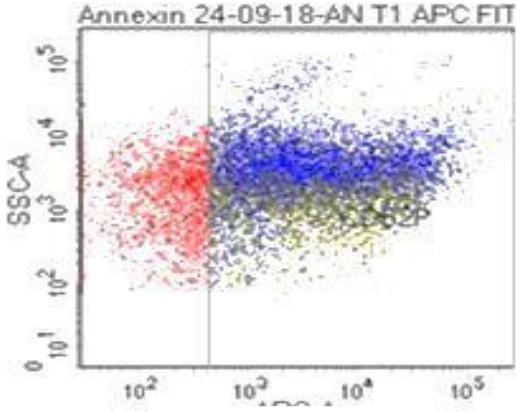

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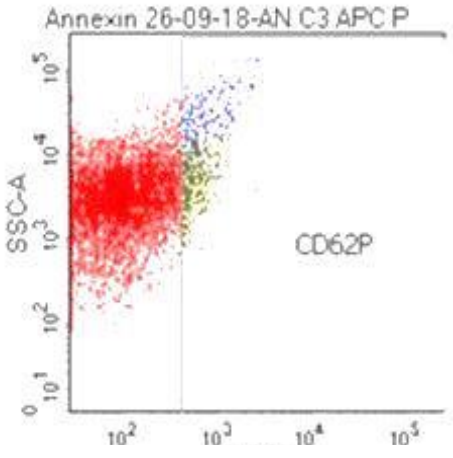

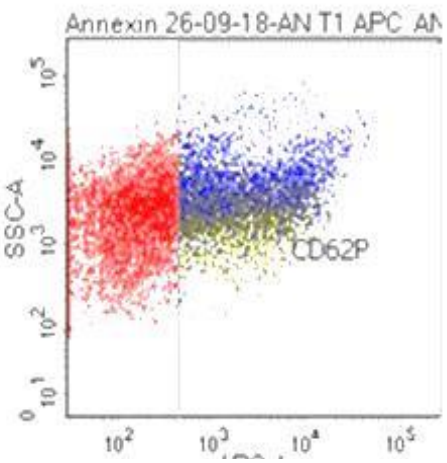

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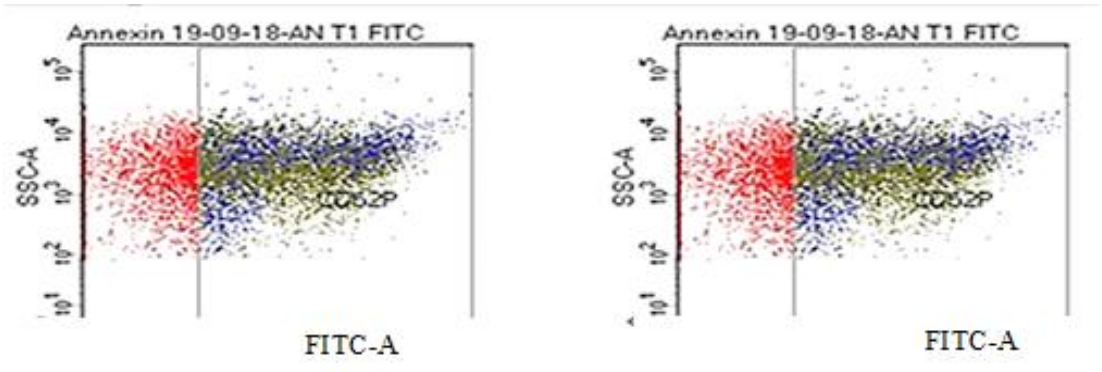
Figure 50(b): MFI for CD62P and Annexin V (phosphatidylserine) **PR-PC without PAS** on day 7(maximum day of storage



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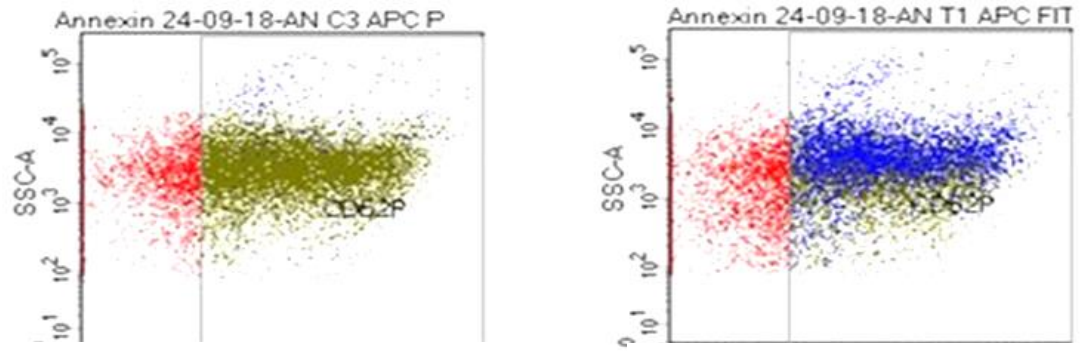

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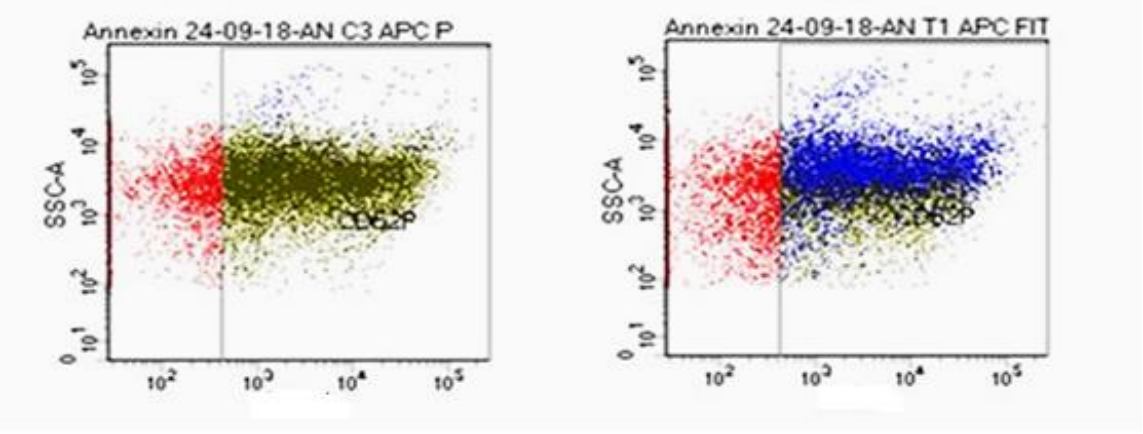

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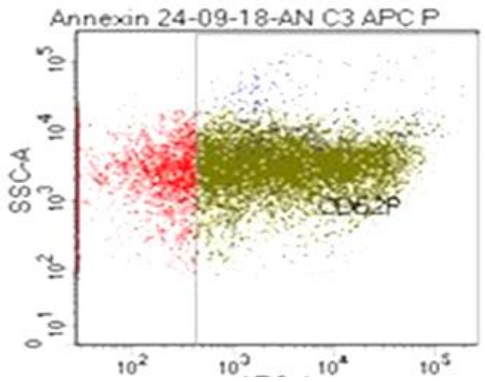
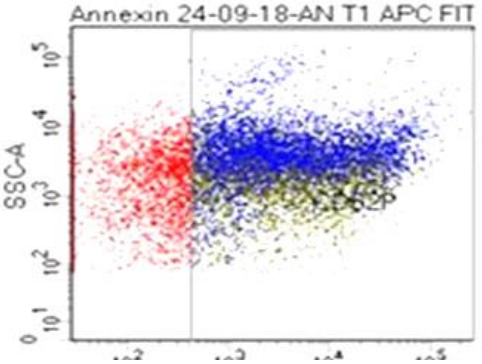
Figure 50(c): MFI for CD62P and Annexin V (phosphatidylserine) **BC-PC with PAS** on day 7(maximum day of storage)





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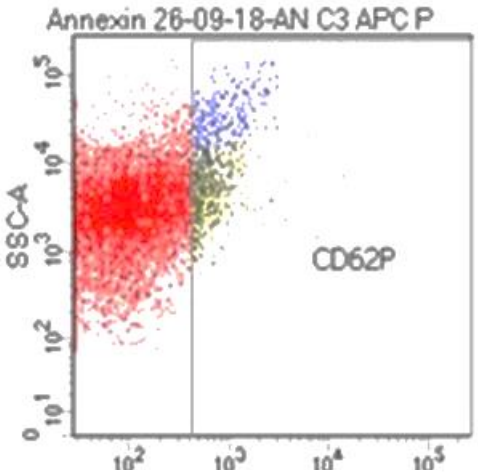

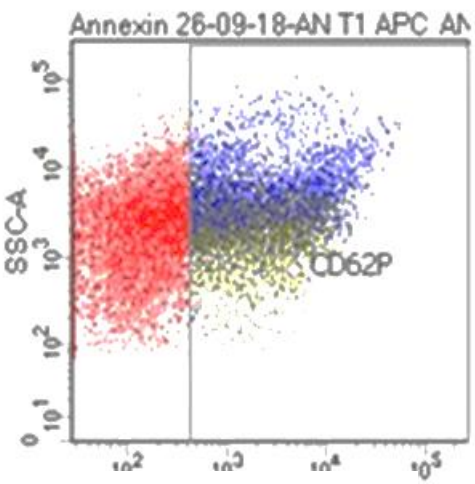

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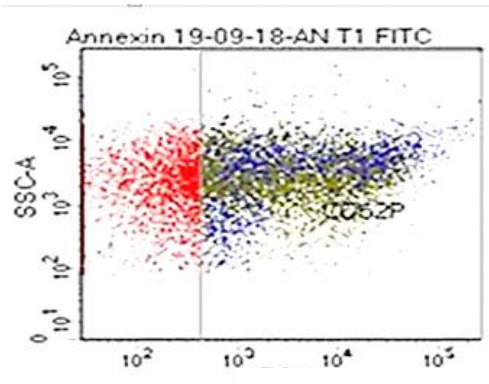

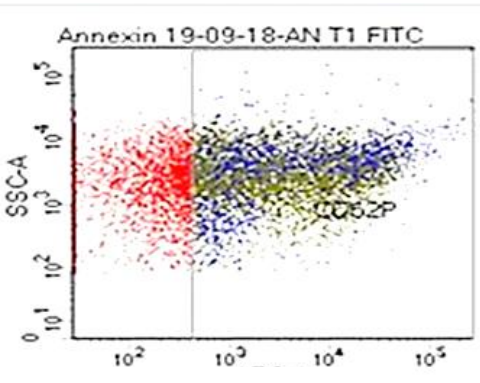

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Figure 50 (d): MFI for CD62P and Annexin V(phosphatidylserine) **BC-PC without PAS** on day 7(maximum day of storage)

Discussion

P-selectin and Annexin V can be detected on the activated platelet. Annexin V was used as a parameter for quality monitoring of PCs during storage. Redistribution of phosphatidylserine (from the inner membrane surface to the exterior surface accompanies during platelet activation.[139] The exposure of PS can be measured by using FC and fluorescent-labeled annexin V. Annexin V was used as a parameter for quality monitoring of platelet concentrates during storage. This assay is based on the principle that annexin V binds to PS, with high affinity and high specificity. Activation of thrombocytes is followed by an increased CD62P expression; this protein is the main component of the alpha granules secreted from the granules during storage.[139]

Our study highlighted the fact that the degree of in vitro activation as evidenced by the expression of CD62P and Annexin V binding were dependent on the different preparative methods.[140] We found that the extent of activation was significantly higher in PRP-PCs than in BCs. It was concluded that, immediately after preparation, PRP derived platelets are more activated than BC-derived platelets. This is most likely a result of the pelleting that follows the second high-speed centrifugation of the PRP.[140]

Although in both preparations, platelet activation is increased by storage time, BCs are characterized by a much better in vitro than PRP-PCs. However, the different CD62P and Annexin V in PRP-PCs and BCs clearly demonstrate that process of activation exceeds that of BCs. Platelets processed by the buffy coat technique showed less P-selectin (CD62P) expression than platelets prepared by the PRP method.[140]
In addition, our study also highlights that the measurement of CD62P and Annexin V may be more useful markers for estimation of activated PCs, since it may be less susceptible to artifactual elevation due to minor variations in sample handling and assay procedures.[139]

Numeric FC data (% of positive cells and MFI values) for total platelets and the platelet sub populations were also studied. For each of the analyzed PC, a specific FSC/SSC gating parameter of total PCs and platelet populations on day 0 was identified and kept it constant during analysis on storage days 5 and 7.[141]

Conclusion

This study shows that the comparative degree of activation of PCs during storage period. However, more FC studies need to be conducted to substantiate our findings on a larger scale.[142] FC of PCs needs to be encouraged because of its numerous advantages namely a) PCs are analyzed in their physiological state. b) insignificant in vitro platelet activation due to minimum manipulation of the sample c) very small amount of blood required d) simultaneous determination of resting as well as activated state of the PCs and e) detection of neo-epitopes expression on the surface of PCs respectively.[142]

Evaluation of the level of expression of various activation markers on different platelet sub populations could be an additional valid analysis in QC of PCs, particularly during the extended period of storage.

CHAPTER 6:
PROTEOMIC ESTIMATION OF STORED PLATELETS

Introduction

Proteomics involve the large-scale study of proteins, their structure and physiological role or functions.

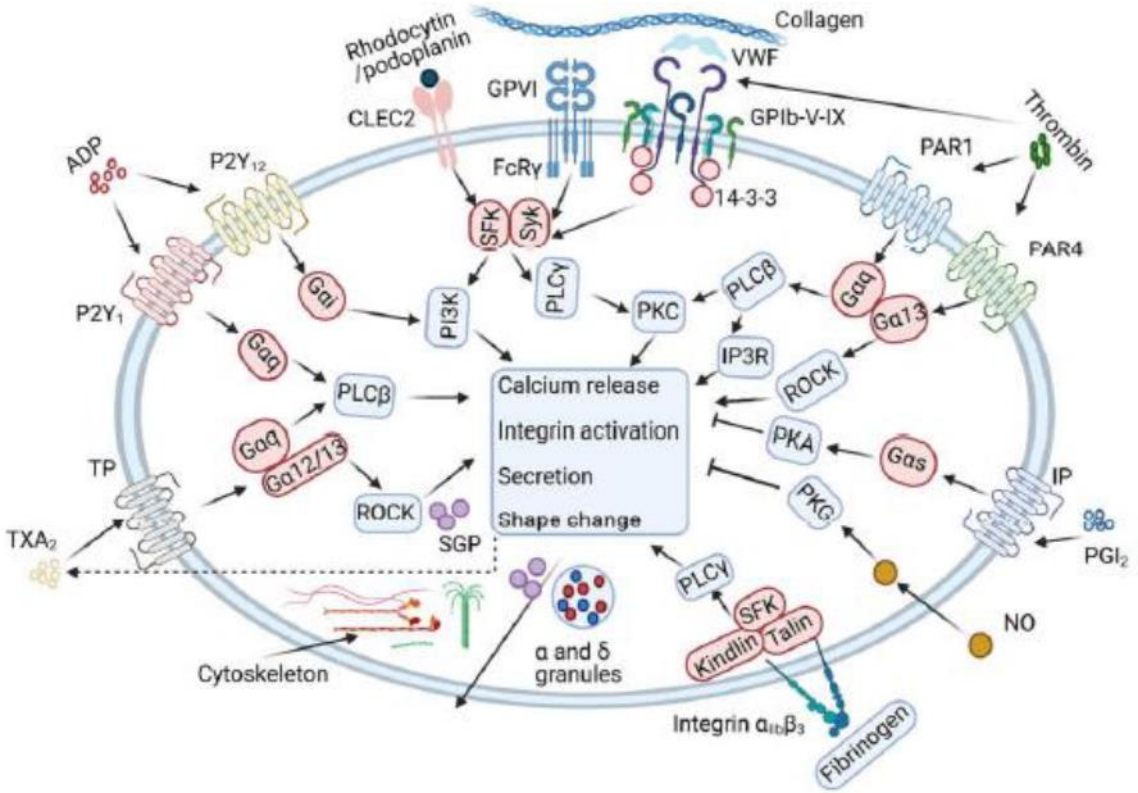

Figure 51 a: General overview of platelet signalling pathways.

Overview of key platelet signalling and responses via key platelet receptors and agonists, examined by platelet proteomic analysis. Indicated are signalling via the collagen receptor glycoprotein (GP)VI, VWF receptor GPIb-V-IX; the proteinase-activated receptor (PAR)1 and PAR4 for thrombin; the podoplanin and rhodocytin receptor C-type lectin receptor 2 (CLEC2); the ADP receptors P2Y1 and P2Y12; thromboxane (TX)A2 mimetic U46619 (pathway inhibited by aspirin);integrinIIb3 outside/in signalling; actin and tubulin cytoskeletons; platelet-inhibiting prostacyclin I2 (PGI2) and nitric oxide (NO); and-granuleand-granulesecretion. Otherabbreviations:G, heterotrimeric G proteins; PKA, PKC, PKG, protein kinases A, C, G; PLC, phospholipase C; SGP, small GTP-binding proteins; SFK, Src-family kinase. **(**adapted from Bhurkhart et al Circ Res 2014;114:1204-19)[146]

The term *proteomics* first appeared in 1997.[143] It was very similar to the word *genome*. The

word *proteome* is actually a combination of *protein* and *genome* and was coined by Mark Wilkins in 1994.[144] To be precise and specific, proteome is the entire complement or database or set of proteins produced by a living organism. Proteomics is the analysis of the entire protein complement of a cell, tissue, or organism under a specific, defined set of conditions. In its present state, it is dependent on decades of technological and instrumental developments. These developments have included advances in mass spectrometry (MS) technology, protein fractionation techniques, bioinformatics, etc. Proteomics relies on three basic technological cornerstones that include a) method to fractionate complex protein or peptide mixtures, b) MS to acquire the data necessary to identify individual proteins, and c) bioinformatics to analyze and assemble the MS data. Proteins are quintessential cellular components or biomolecules in any living organism.

Proteomics analysis actually begins at the end of the sample preparation. Protein species undergo an analytic step which separates them on the basis of their biochemical/ physical properties (e.g. molecular weight, isoelectric point, mass/charge ratio). This analytic phase mainly relies on gel-based approaches (mono- or bi-dimensional electrophoresis) and chromatographic methods. Separated protein spots are then cut from the gels and trypsinized (thus cleaved into peptides) or directly chromatographically eluted to a mass spectrometer for protein/peptide identification (also known as peptide mass fingerprinting). The protein from which these peptides were derived is determined upon mass spectrometric identification by comparing the obtained sequence with theoretical mass predictions of "known" protein sequences from the database.[146]

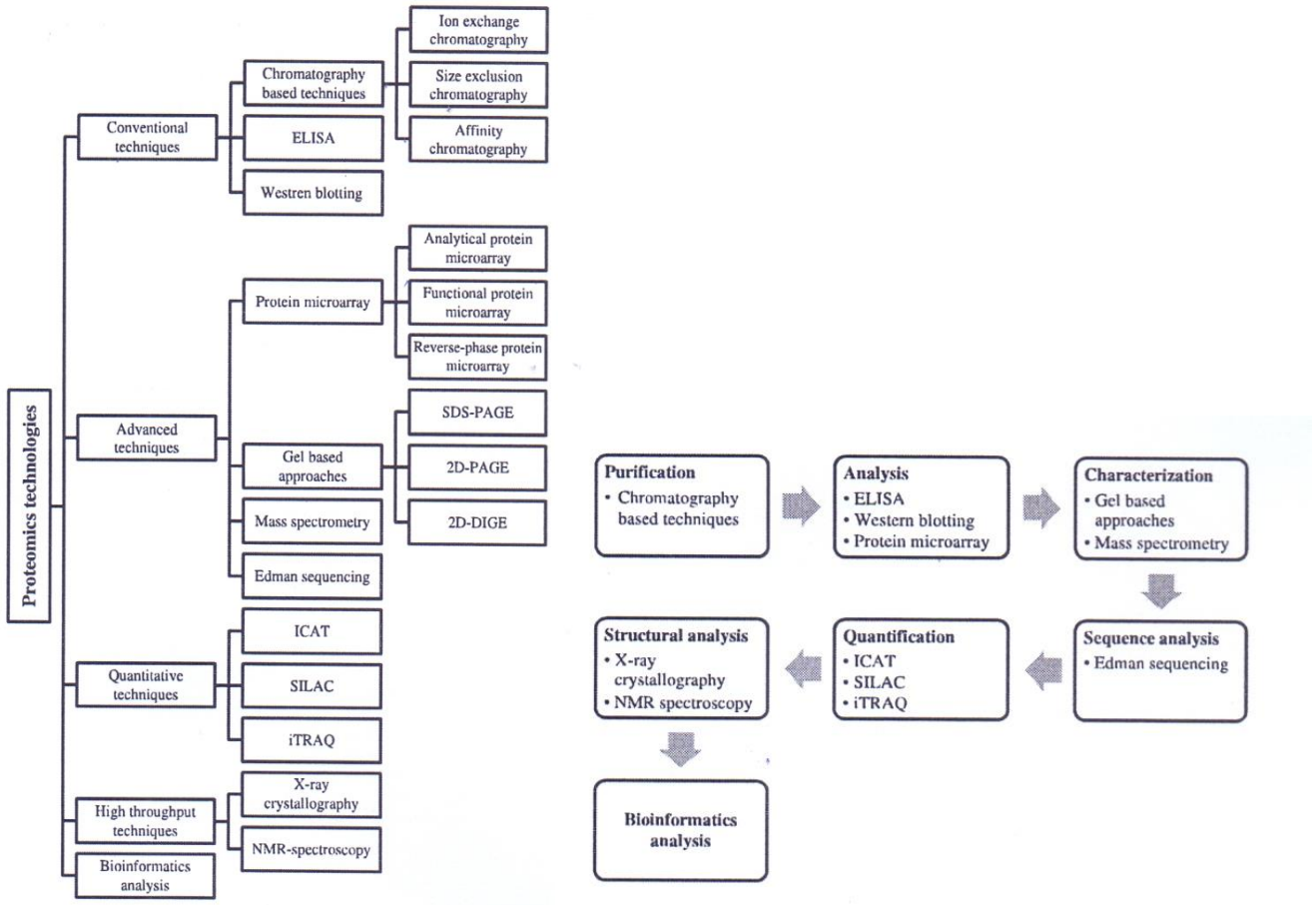

Figure 51 b: An overview of proteomics techniques techniques **(**adapted from Bhurkhart et al Circ Res 2014;114:1204-19)[146]

Figure 51 c: Applications of proteomics **(**adapted from Bhurkhart et al Circ Res 2014;114:1204-19)[146]

Aim and Objectives

1. To study proteomic expression among PCs suspended in plasma during extended storage period.
2. To study proteomic expression among PCs suspended in PAS during extended storage period.

MATERIALS AND METHODS:

Proteomics tries to determine the whole protein profile of a specific sample under analysis. Proteomics analyses of blood and blood components definitely represent a challenging task.

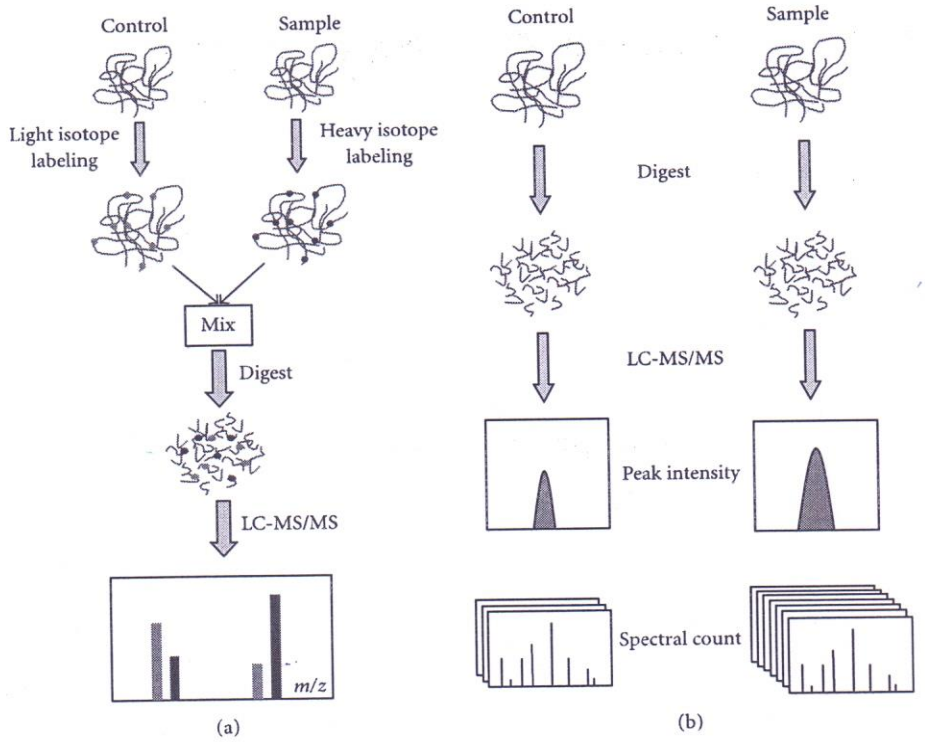

Figure 52: General approaches of quantitative proteomics. (a) Shotgun isotope labelling method. After labelling by light and heavy stable isotope, the control and sample are combined and analysed by LC-MS/MS. The quantification is calculated based on the intensity ratio of isotope-labelled peptide pairs. (b) Label-free quantitative proteomics. Control and sample are subject to individual LC-MS/MS analysis. Quantification is based on the comparison of peak intensity of the same peptide or the spectral count of the same protein. (adapted from Maguire PB et al 2:642-648,2002)[147]

Reagents and materials

Blood samples were collected from 20 blood donors with age, gender and body weight matched controls. Liquid chromatography–mass spectrometry (LCMS) grade solvents 0.1% formic acid in water, 0.1% formic acid in acetonitrile and trypsin enzyme were purchased from Pierce™ (Thermo Scientific Pierce™, USA). The other solvents like LCMS grade water and acetonitrile were obtained from J T Baker™. The chemicals for protein digestion, dithiothreitol, iodoacetamide, urea, thiourea and ammonium bicarbonate were purchased from Sigma-Aldrich™. The chemicals required for PAS, trisodium citrate dihydrate, sodium acetate trihydrate, sodium hydrogen phosphate, disodium hydrogen phosphate, sodium chloride, potassium chloride and magnesium chloride hexahydrate were also purchased from Sigma-Aldrich™. Sodium dodecyl sulfate, tris-HCl and EDTA for lysis buffer were

obtained from Bio-Rad™. Human α–Thrombin (Factor IIa) (catalog#: HT 1002a, Size: 1000units) was from Enzyme Research Laboratories™ (South Bend, IN, USA) BC-PC was prepared from WB as per the SOP, for PCs purification and ex–vivo activation with thrombin for proteomic analysis.

PCs were washed twice with the Tyrode's Buffer containing 134mM NaCl, 12mM $NaHCO_3$, 2.9mM KCl, 0.34mM Na_2HPO_4, 1mM MgC_{l2}, and 10mM Hepes (pH 7.4) and centrifuged at 750xg for 10 minutes. To obtain thrombin activated PCs, washed PCs were re-suspended in 0.5mL of washing buffer with 1.8mM $CaCl_2$ (to have $2x10^8$ PCs/ ml) and treated overnight with 1 IU of human alpha–thrombin for each sample.

PCs treatment with PAS and proteins extraction

A set of pooled thrombin activated platelet concentrate was prepared and was segregated into two equal halves. One half of the PC was re-suspended in 65% of (PAS; SSP +) and the other half was kept without PAS. PAS was composed of trisodium citrate dihydrate (3.18 g), sodium acetate trihydrate (4.42 g, sodium hydrogen phosphate (1.05 g), disodium hydrogen phosphate (3.05 g), sodium chloride (4.05 g), potassium chloride (0.37 g) and magnesium chloride hexahydrate (0.3 g). Both sets of PCs were stored at 20^0C – 24^0C for 9 days according to transfusion medicine guidelines. Protein extraction was done by employing the PCs cryogenic lysis using 5 cycles of freezing in liquid nitrogen and thawing at 37^0C followed by centrifugation at 18,000 rpm for 30 minutes at 4^0C. Pellet was re-suspended in 50 mM ammonium bicarbonate buffer (pH 8.5) containing 8M urea and sample was stored at -20^0C until further LC-MS/MS analysis.

Protein tryptic digestion

The protein pellets were dissolved in urea buffer (8M urea/2M thiourea) and the concentration of the samples were estimated using (NanoDrop™ 2000/2000c).

Protein samples were reduced with 10 mM DTT and incubated at 37^0C for 30 minutes followed by addition of 30 mm IAA(Iodoacetamide) kept and incubated in the dark (RT, 30 minutes) to alkylate the free cysteine residues. The samples were diluted to 1M urea prior to the addition of trypsin (1:50 (w/w)). Sample was kept at 37^0C for overnight digestion. Final concentration of 0.1% formic acid was used to quench the reaction. The digested peptides were dried under vacuum and desalted using C-18 ziptip (Pierce C18 Tips, 10 µL bed). The eluted peptides were dried and re-dissolved in 2% acetonitrile/0.1% formic acid.

LC-MS (liquid chromatography-mass spectrometry) Analysis

The analysis was carried out in Thermo Orbitrap™ fusion tribird mass spectrometer coupled with an EASY-nLC 1200 ™ series system. The peptides were injected onto reverse-phase C18 pre column (Acclaim PepMap 100 C18 ™ 3 µm, 75 µm × 2 cm nanoviper) and then separated on C18 analytical column (Easy spray Pep map RSLC C18 ™ 2µm, 15 cm × 75 µm) for a resolved separation. Peptides were eluted using a linear gradient of 168 minutes from 5% to 45% solvent B (80% acetonitrile in 0.1% formic acid) at a flow rate of 300 nL/min, 45% B to 98% B for 12 minutes and solvent A composition was 0.1% formic acid in LC grade water.

The mass spectrometer was operated with a positive ionization voltage of 1900 V and 27^0C temperature was used for ion transfer tube. MS spectra were acquired in the Orbitrap ™ with a resolution of 120000 over a mass range of 375-1700 m/z, automatic gain control (AGC) value was set to 4.0 e5 and a maximum injection time was kept as 50 minutes. 20 highly intense ions for fragmentation was selected by Top-Speed acquisition mode which were isolated by quadruple with an isolation width of 1.2 Da. These ions with charge states ranging from 2+ to 7+, were fragmented by HCD with an optimized collision energy of 30% with step energy ±5. The fragmented ion spectra were acquired by ion trap in centroid mode, AGC value was set to IE4 (regulatory protein) and a maximum injection time of 35 seconds was used. The data acquisition was done with Excalibur ™ software (version- 4.1.31.9).

The following illustration exhibits assessment of specific peptides and proteins in proteomic cell lysates.

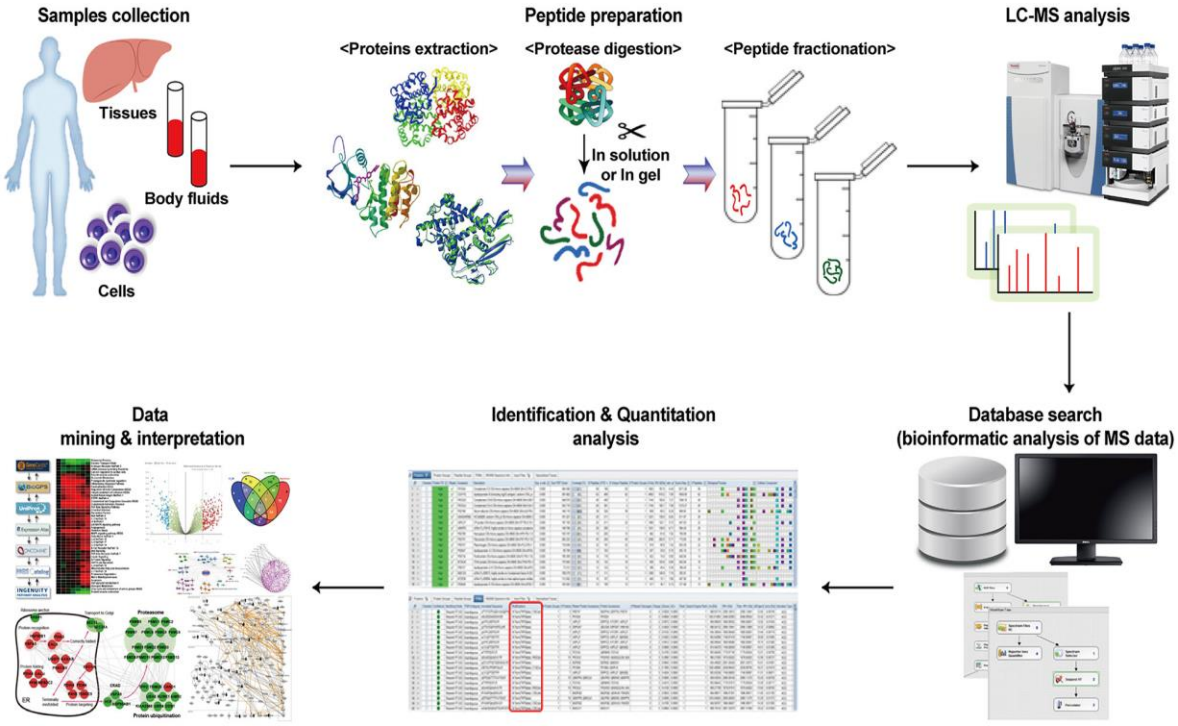

Figure 53 (a): Proteomics workflow based on LC-MS Figure A (1-4) shows protein extraction along with enzymatic digestion to assess PTM Figure 6 b) Pooling of samples Figure 7(b) LCMS data analysis. Figure 8 b) Isotope labeling what can proteomics tell us about PCs. (adopted from Yang Woo Kwon et al. 2021;8:747-52)[148]

Data Analysis

Raw data files were processed into Mascot Generic Format (MGF) peak list by using Proteome Discoverer ™ (version 2.1). MGF peak list was further analysed against human proteome database (Downloaded from Uniprot on 2018) by Mascot Daemon ™ (version 2.6). A mass tolerance of 10 ppm was used for the precursor ions and 0.6 Da for the fragmented ions. Maximum missed cleavages were allowed up to two; "Trypsin" was set as enzyme specificity and charge states were set to 2+, 3+ and 4+. The fixed modification was set as carbamido-methylation at cysteine whereas the dynamic modification was set as Oxidation at methionine. A False Discovery Rate (FDR) of 1% was utilized for both protein and peptide estimation. emPAI based Label Free method was used to quantitatively compare the effect of PAS treatment on PCs.

Results:

Proteomics based on mass spectrometry (MS) is an innovative practice that can identify proteins with exquisite precision and sensitivity. The mass spectrometry method coupled with liquid chromatography aids in the quantification of thousands of protein expressions and helps to analyze the dynamic proteome changes occurring in a particular condition. It provides extensive knowledge of the proteins expressed differentially in a particular condition. The analysis of differential expression helps to provide useful information about the molecular behavior of a particular condition of the disease and aids in biomarker development.

P – Platelets with additives
WP – Platelets without additives
N – 129 N - 150

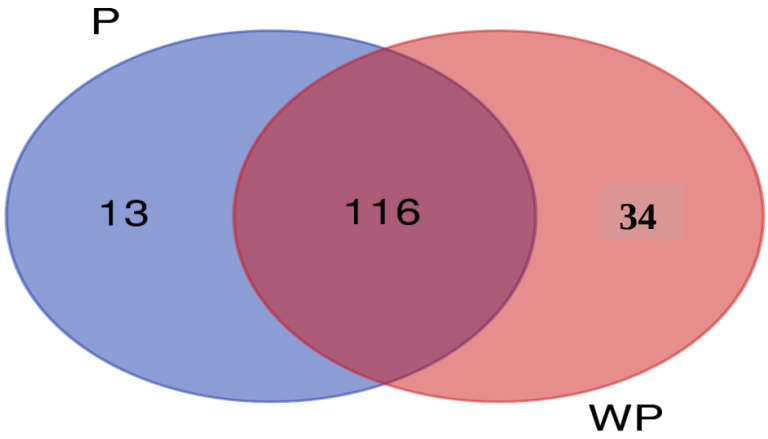

Figure 54: Venn diagram: Showing expression of platelet proteins suspended in PAS (P-13) and also showing expression of platelet proteins suspended without PAS (WP-34)

A Venn diagram is an illustration that uses circles to show the relationships among things or finite groups of things. Venn diagrams help to visually represent the similarities and differences between two concepts.

Differential expression based on proteomics technologies to detect, identify, and characterize proteins on a wide scale makes it a highly promising biomarker discovery tool for various diseases. The identification of protein biomarkers from biological samples can be rarely detected through traditional methods like two-dimensional (2D) gel electrophoresis due to their low abundance. Therefore, proteomics techniques based on gel-free or mass spectrometry approaches are considered to be the best choice for measuring protein levels with increased sustainability and reproducibility.

Table 41 : Expression of platelet proteins suspended in PAS along with their respective storage period.(Refer master chart 1(a), 2(a) and 3(a))

Protein ID	Protein Description	Storage Period	Functions
P02747_C1QC	Actinin	Day 0	Participates in protein-protein interaction[149]
P01031_CO5	Complement C5	Day 0, 7	Complement activation[150]
F5H1C6	Fermitin family homolog 3(Fragment)	Day 7	Platelet adhesion[151]
A0A087X232	Component C1s subcomponent	Day 5	Complement activation[152]
P08185_CBG	Corticosteroid-binding globulin	Day 5	Acute-phase protein' in inflammatory response[153]
A0A286YEY1	Immunoglobulin heavy constant alpha 1 (Fragment)	Day 7	Complement activation[154]
P04217_AIBG	Alpha -1B- glycoprotein	Day 7	Acute phase protein[155]
P06702_ S10A9	Vinculin	Day 0	Cytoplasmic actin-binding protein[156]
P08514-2_ITA2B	Isoform 2 of Integrin alpha-IIb	Day 0	Platelet agrregation[157]
P35908_K22E	Keratin, type II cytoskeletal 2 epidermal	Day 0	Maintenance of cellular integrity and cell growth[158]
Q7Z2Y8_GVIN1	Interferon-induced very large GTPase 1	Day 0, 7	Cell inflammation and immunity[159]
A0A0G2JPR0	Complement C4-A	Day 0,5,7	Complement activation[160]
K7EQQ3	Keratin, type I cytoskeletal 9	Day 0,5,7	Structural integrity[161]

Table 42: Expression of platelet proteins suspended in without PAS along with their respective storage period.(Refer master chart 1(b), 2(b) and 3(b))

Protein ID	Protein Description	Storage Period	Functions
A0A075B6S6_KVD30	Immunoglobulin kappa variable 2D-30	Day 5,7	Immune response[162]
P00488_F13A	Calpain	Day 0,5,7	Cell signalling[163]
P00739_HPTR	RAP-1	Day 0,7	Cell signalling[164]
P01780_HV307	Caldesmon	Day 5,7	Actin binding protein[165]
P29622_ KAIN	Kallistatin	Day 0,5	Cell regulation[166]
P35858-2_ALS	Isoform 2 of Insulin-like growth factor-binding protein complex acid labile subunit	Day 0,5,7	Cell signalling[167]
A0A024R6I7	Alpha-1-antitrypsin	Day 0,5,7	Acute phase reactant[168]
A0A2R8Y7R2	Pleckstrin	Day 0,5,7	Cell signalling[169]
F5H2D0	Clusterin	Day 0,5	Cell signalling[170]
Q60FE5	Filamin-A	Day 0,5,7	Cell translocation and cell shape[171]
A0A0A0MS15|HV349	Integrin linked kinase	Day 0,5,7	Connection of integrins to the actin cytoskeleton and signalling pathways[172]
P00450|CERU	Cyclophilin A	Day 0,5,7	Regulation of protein activity[173]
A0A0C4DH33_HV124	78-kd glucose dependent protein	Day 0,7	Regulation of protein synthesis[174]
A0A0C4DH41_HV461	Septin-2	Day 5,7	Regulation Cytoskeleton[175]
O14791-2_APOL1	Isoform 2 of Apolipoprotein L1	Day 0,7	Cell transport and metabolism[176]
P05160_F13B	Talin	Day 0,7	Communication between actin and cell matrix[177]

Protein ID	Protein Description	Storage Period	Functions
P02747_C1QC	Osteonectin	Day 0,5,7	Collagen-binding matricellular protein[178]
P01031_CO5	Thrombospondin	Day 0,7	Regulating cell–cell and cell–matrix interactions[179]
F5H1C6	Fermitin family homolog 3(Fragment)	Day 7	Cell adhesion[180]
A0A087X232	CXCL-7	Day 0,5	Immune regulation[181]
P08185_CBG	Von-willebrand factor	Day 0,5,7	Platelet aggregation [182]
A0A286YEY1	Immunoglobulin heavy constant alpha 1 (Fragment)	Day 0,5,7	Protein regulation[183]
P04217_A1BG	Alpha-1B-glycoprotein	Day 5,7	Protein regulation[184]
B4E1Z4|B4E1Z4	Myosin	Day 0,5,7	Intra cellular signalling[185]
Q5T0R1|Q5T0R1	Adenylyl cyclase-associated protein 1 (Fragment)	Day 0,5,7	It regulates actin cytoskeleton and the Ras/cAMP pathway[186]
P19438-5|TNR1A	F-actin capping protein	Day 0,7	It helps in Polymerization of actin filaments[187]
J3QSE5|J3QSE5	Phosphatidylcholine-sterol acyltransferase (Fragment)	Day 0,7	Protein metabolism[188]
Q5H928|Q5H928	3-hydroxyacyl-CoA dehydrogenase type-2	Day 0,5,7	Protein metabolism[189]
P27105-2|STOM	Calmodulin	Day 5,7	Signalling pathways[190]
G3V264|G3V264	Plasma serine protease inhibitor (Fragment)	Day 5,7	Helps in protein protein Interaction [191]
D6RAR4|D6RAR4	ARP-2/3	Day 0,7	Helps in cell-cell and cell matrix interaction[192]
P00748|FA12	Protein 14-3-3	Day 5,7	Cell signaling pathway[193]
P05543|THBG	Fibrinogen	Day 5,7	Formation of fibrin plug[194]
A0A2R8Y6G6|A0A2R8Y6G6	Gelsolin	Day 5	Actin-remodeling protein[195]

Results are being discussed in following table.

Differential Expression Profile (Refer Table 41,42)

Proteomic expression of stored PCs with PAS on day 0	Master chart 1(a)
Proteomic expression of stored PCs without PAS on day 0	Master chart 1(b)
Proteomic expression of stored PCs with PAS on day 5	Master chart 2 (a)
Proteomic expression of stored PCs without PAS on day 5	Master chart 2 (b)
Proteomic expression of stored PCs with PAS on day 7	Master chart 3 (a)
Proteomic expression of stored PCs without PAS on day 7	Master chart 3 (b)
Differencial expression of proteins. The top 47 upregulated and down regulated proteins in storage period.	Master chart

Discussion

Recently, proteomic technology is being increasingly applied for research of platelet proteins leaving to the emerging of 'platelet proteomics' which is of great clinical significance.[196]

Sored PCs produced pro-thrombotic pro-inflammatory mediators which are responsible for the onset of PSL and ATR. Technological innovations such as 2-D gel electrophoresis and LC-MS based proteomic investigations have been utilized to discover the molecular mechanism associated with protein alterations in PCs during storage.[197]

Understanding platelet proteomics remains a challenge because of certain limitations which includes standardization and validation of proteomic technics including PC preparation, protein extraction separation and analysis.

Platelet proteomics involves huge financial outlay technological complexities along with extremely skilled man power. In order to obtain optimum results platelet proteomics requires excellent team work between basic researchers, clinicians and statisticians.[198]

The proteome is the pool of proteins expressed at a given time and circumstance. The word "proteomics" summarizes several technologies for visualization, quantitation and identification of these proteins. Recent advances in these techniques are helping to elucidate platelet processes which are relevant to bleeding and clotting disorders, transfusion medicine and regulation of angiogenesis.[199]

Detailed knowledge of the protein composition of platelets and the differences compared with nucleated cells is, therefore, essential to improve our understanding of the delicate equilibrium between platelet inhibition and activation. Platelets are isolated from either freshly donated blood or leukocyte-depleted stored platelet concentrates. Whereas the latter is more convenient, fresh blood donations are preferable to ensure that the sample is as close to the *in vivo* situation as possible.[200]

For high reproducibility and confidence of the generated data, it is important to monitor the entire workflow including (1) patient selection, (2) blood drawing, (3) platelet isolation and purity, (4) lysis and proteolytic digestion, along with analytic steps such as (5) chemical labeling, (6) prefractionation of the peptide mixture, (7) LC-MS analysis, and (8) MS data interpretation.[197]

It is important to realize that platelets and their protein/RNA content are susceptible to manipulation and can easily be influenced during blood collection and processing.[197] Hence, it is essential to use standardized blood collection, sampling and preparation techniques in order to minimize the risk ex vivo platelet activation as done in the current study.

Age and gender can significantly influence platelet characteristics and therefore, age and gender matched control group selection is required and the same has been adhered to in the study.

In the current study LC-MS approach has been used which has several advantages[199] including (1) availability of improved mass spectrometers providing higher sensitivity, specificity and speed (2) better high performance LC systems and materials providing an enhanced separation of highly complex samples; and (3) novel bioinformatics strategies enabling highly complex data interpretation at well-defined quality measures. In addition, the use of the state-of-art LC-MS technique in our study has enabled us to have a better data collection and interpretation with a well-defined FDR of 1% which results in improved validation of the results.

At present, the quality of PCs is primarily determined in vitro by selective methods, such as swirling assessment, pH determination, flow cytometry or aggregometry, which can provide only limited information regarding PLT function or morphology.[201] Proteomics could potentially become a powerful tool for quality control analysis of PLTs during storage in clinical practice by evidencing the molecular alterations which take place within stored units.

Proteomics methods could be suitable to evaluate proteins which accumulate in the supernatants during storage [202] and are thus related to a series of pro-inflammatory events which are triggered upon long-stored PLT transfusion. In a study conducted by Liumbruno GM et al[203] a series of cytokines (commonly implicated in allergic responses), such as BDNF, CCL5, PDGF as well as clusterin (a complement-mediated lysis inhibitor), TLT-1 (having a role in PLT adhesion) and ILK (aggregation and adhesion to damaged endothelium) were found to increase in the supernatant after 7 days of storage, suggestive of progressive leakage from or degradation of PLTs during storage. These findings are relevant in light of the current discussion around the safety and efficacy of extending the shelf-life of PCs to 7 days instead of the present 5-day expiry.[204]

Studies done by Anderson NL et al [205] revealed that PSL is characterized by increased release of alpha-granules and cytosolic proteins, increased procoagulant activity, and altered glycoprotein expression. In addition both beta-actin and septin2 were found to be altered by storage highlighting the importance of cytoskeletal reorganization and apoptosis in the PSL which represent novel signaling pathways and future therapeutic targets, as well as potential biomarkers.[206]

Concerns have so far only addressed the increased risk of bacterial growth, proportional to the prolongation of the storage. Longer-stored PLTs actually display a higher proinflammatory capacity, even when leukoreduced, which may correlate to the persistence of adverse transfusion reactions such as FNHTR thus nullifying the efforts for a quantitatively improved storage.[207]

Recent studies have adopted complementary proteomics approaches to monitor PLT storage lesions from day 1 to 7 of storage.[208] These approaches were referred to as protein-centric or peptide-centric, since they addressed the single molecules or protein aggregates/complexes, respectively.[209]

Recent review of literature show no available study on platelet proteomics conducted in this part of the region. Our study was a maiden attempt to identify and assess the platelet proteins with and without PAS during the extended the storage period. We have identified a total 34 proteins during the extended storage period.

Future perspectives and challenges ahead

In the recent past, platelet proteomics has rapidly evolved from the early days of 2D-Gel electrophoresis to the latest LCMS techniques which has enabled quantitative estimations of proteins along with their regulatory pathways leading ultimately to gradual enlargement of human molecular platelet proteome.[210]

However, certain challenges remains to be addressed as platelet proteomics progresses from basic protein discovery towards more complex issues such as post translational modifications, (PTM), identification of multiple protein regulatory pathways etc.[211] Hence there is a urgent need for more details study with standardization of laboratory research protocol. The current study is one such step in that direction. However, the analysis of protein changes during platelet storage comprised the differences in the pattern between day 1 to day7 and further analysis are necessary to determine more detailed information using a day to day assessment because the actual levels of protein may be more dynamic and reflect the summation of de novo synthesis and degradation.[211]

Proteomic experiments can provide data about localization, interactions, posttranslational modifications, and activation states of gene products. On its own, proteomics can pinpoint target proteins, but it is important to consider that conclusions can only be clear and strong at validated combinations of (1) study design, (2) platelet preparation, (3) proteomic sample preparation, (4) LC-MS analysis, and (5) MS data interpretation. Hence, our study highlights

the fact that proteomics provides an excellent tool to decode complex processes by identifying novel platelet-expressed proteins and analyzing functional changes of the platelet proteome.[197]

However, emphasis should be laid on proper standardization and validation of the procedure involved towards proteomic study. Similarly efforts must be made to minimize pre-analytical interferences due to various causes including the procedural impurities**.**

Conclusion

As PCs are anucleate with limited protein synthesis. Proteomics provides excellent mechanism to decode complex compounds by identifying novel platelet-expressed proteins, dissecting mechanisms of signaling or metabolic pathways, and analyzing functional changes of the platelet proteome.

Platelet proteomics is a relatively young field of research which provide certain unique challenges and opportunities as well blood platelets are involved in several pathologies, beyond their fundamental role in primary hemostasis. Platelet proteomics represents an efficient tool to help elucidating platelet biology, being genomic and transcriptomic studies limited by the absence or limited amount of DNA and mRNA, respectively.

Current study highlighted the advantage of using standardized protocol for platelet protein extraction and expression along with the benefits of using LC-MS level free quantification method which has provided powerful tool for analyzing protein with greater validity.

The present study has identified the various platelet proteins expressed in PAS and without PAS along with their levels of expression and shows that even under difficult analytical conditions, platelet proteomics is able to produce meaningful and consistent results. We are at the beginning of a new era for platelet proteomics and its application to the study of platelet related diseases. This new era will hopefully increase our knowledge of platelet disorders and improve their diagnosis.

However this basic study needs to be further complemented with more detailed analysis of various other proteomic aspects including glycosylation phosphorylation and post-translational modifications (PTM) etc. The findings of the study can act as a basis on which further improvement can be done.

Despite these limitations, proteomics, when combined with other complementary technologies such as molecular biology, has enormous potential to provide new insight in to various aspects of platelet metabolic.

SUMMARY

Summary

Platelet inventory management possess certain unique challenges because the PCs are perishable blood product with a extremely short shelf life and because of huge clinical demand it often results in serious platelet inventory management problem characterized by frequent out dating, high rates of wastage coupled with inadequate clinical supplies associated with serious health, financial and ethical consequences. Hence the objective of our study was to develop certain strategies with the involvement of all the stakeholders to explore the feasibility of extending the shelf life of PCs to overcome the challenge.

In the current study we have adopted several novel approaches for extending the PCs shelf life which includes the comparative evaluation of PCs of various preparation methodologies along with the morphological indices which can perform as quality indicators of stored PC even during the extended storage period. Present study proves that morphological indices are useful screening test for evaluation of PSL because they are simple, convenient and cost effective. In addition, various metabolic investigations along with molecular diagnostic tools such as flow cytometry studies and proteomic analysis utilized un the current study have broadly suggested that various quality parameters are satisfactorily maintained in the platelets during the extended period of storage which can be corroborated further in future studies.

As noted in our study extension shelf life of platelets is not only desirable but is also feasible because of the availability of newer and better technologies. However, certain measures needs to be taken to meet this challenge effectively in order to resolve certain unanswered questions including a) better standardization of recent intervention methods b) promotion of point of care testing (POCT) and PAS c) implementation of good laboratory practices, quality improvement and quality assurance programs, stringent donor section criteria and waste reduction strategies. All this measures will be useful to clarify various issues regarding extension of the shelf life of platelets and effectively solve new issues/ questions and challenges regarding the same.

The present study has contributed towards the understanding of underlying mechanisms responsible for the onset of PSL and in developing platelet storage regiments which can complement current storage technologies and together, they may achieve a more efficacious and safer protocol for longer term platelet storage. However, more such studies are required in near future to further substantiate our findings.

LIMITATIONS

Limitations

1. Current study is a uni-centric study conducted in blood center attached to a rural tertiary care teaching hospital.
2. Apheresis platelets have not been included in scope of the study.
3. Utilization of Leuco-filtered blood bags needs to be included.
4. Feasibility of including NAT (Nucleic Acid Testing) to rule out TTI needs to be considered.
5. Extensive *In-vivo* studies with PAS needs to be done.
6. Inclusion of more markers during FC estimation can be considered.
7. Regarding proteomics further standardization needs to be considered.
8. Measures to ensure easy availability of capital and highly skilled technical personnel needs to be done for proteomic study.

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ANNEXURE - I

INFORMED CONSENT FORM

Title: Extension of Shelf Life of Platelets; Prospects and Pitfalls.

I have read or read to me and understand the purpose of this study and confidential nature of the information that will be collected and disclosed during the study.

I understand that I remain free to withdraw from this study at any time. Participation in this study does not involve any extra cost to me.

I have had the opportunity to ask my questions regarding the various aspects of this study and my questions have been answered to my satisfaction.

I, the undersigned agree to participate in this study and authorize the collection of 450 ml of blood sample and disclosure of my personal information as outlined in the consent form. Further the sample will be stored and used in the future after informing the patient.

Participant's name and signature Date

Signature of the witness Date

Signature of the investigator Date

ANNEXURE-II

BLOOD DONOR INFORMATION SHEET

Title: Extension of Shelf Life of Platelets; Prospects and Pitfalls.

Introduction: My name is:

Consent for the interview:

PLACE : R.L Jalappa Hospital, Blood Center, Sri Devaraj Urs Medical College ,Kolar.

The main aim of the study is to explore the feasibility of extending the shelf life of platelet in order to meet the clinical requirements and reduce the wastage of this precious resources.

You are requested to participate in a study conducted by the department of Pathology as a part of thesis work. This study will be done on whole blood derived human platelets. The specimens will be collected at R.L Jalappa Hospital blood center attached to Department of Pathology, Sri Devaraj Urs Medical College, Kolar.

The information collected will be used only for dissertation and publication. There is no compulsion to agree to participate. You are requested to sign / provide thumb impression only if you voluntarily agree to participate in the study. All information collected from you will be kept confidential and will not be disclosed to any outsider. Your identity will not be revealed. You will not receive any monetary benefits to participate in this research.

This informed consent document is intended to give you a general background of study. Please read the following information carefully and discuss with your family members. You can ask your queries related to study at any time during the study. If you are willing to participate in the study you will be asked to sign an informed consent form by which you are acknowledging that you wish to participate in the study and entire procedure will be explained to you by the study doctor. You are free to withdraw your consent to participate in the study any time without explanation and this will not change your future care. For any clarification you are free to contact the investigator.

For any clarification please contact the following

Investigator: Name: Dr. Subhashis Das

Department of Pathology, SDUMC, Kolar. **Contact Number:** 8217570123

ANNEXURE – III (STANDARD PROFORMA)

Title: Extension of Shelf Life of Platelets; Prospects and Pitfalls.

Name:

Age:

Gender:

Contact details with phone & email ID:

Occupation:

Donor examination: Body weight Hb Platelet count(%)

Donor deferral: Yes/No

Investigations; 0, 5 and 7 days

1. Morphological parameters;- PLT count: WBC count: RBC count: Etc:
2. Metabolic investigations;- pO_2: pCO_2: Lactate: Glucose: Etc:
3. Bacterial investigations;- Swirling grades: pH: Culture findings: Etc:
4. PAS findings;-
5. Flow cytometry assay;-
6. Proteomics;-

Management and Outcome:

R. L. JALAPPA HOSPITAL & RESEARCH CENTRE BLOOD BANK

TAMAKA, KOLAR-563 103.

Licence No.: KTK/28C-348/2018

BLOOD DONOR QUESTIONNAIRE REGISTRATION AND CONSENT FORM

To ensure your safety as a blood donor and the safety of the patients who will receive your blood, please read the information leaflet provided and answer this questionnaire correctly. If you have any difficulty in filling this form please ask for help from the Blood Centre Staff. All details given by you will be kept confidential

Donor's Name:.....S/D/o.....

Aadhar No.:.....Date of Birth:....., Age:....., Gender : M / F, Contact No.:.....

E-mail:..... Occupation :.....

Address:.....

Tick wherever appropriate [✓]

1.	**Have you donated Blood previously?**		**Yes**	**No**
1.1	If yes how many times	1.2 Date of last donation		
1.3	Did you experience any ailment, difficulty or discomfort during previous donations?		Yes	No
1.4	If yes what was the difficulty?			
1.5	Have you ever been advised not to donate blood?		Yes	No
2.1	Are you feeling well today?		Yes	No
2.2	Have you eaten anything in the last 4 hours?		Yes	No
2.3	After donating blood do you have to engage in have work, driving heavy vehicles/work at heights today?		Yes	No
3.	**Have you had/have any of the following? If yes, discuss with the doctor present:**			
• Allergy • Cancer • Fainting attacks • Heart disease • Lung disease • Asthma • Thyroid Disorders • Leishmaniasis • Autommune disease • Risk Behaviour • Residents of other Countries	• Kidney disease • Mental illness/Schizo phrenia • Amoebiasis • Cold/Cough/Flu/ sorethroat/acute sinusitis • Liver disease • Hemoglobinopathies • Recipient of organ, stem cell and tissue trans plants • Shortness of Breath	• Endocrine disease • Diabetes • Syphillis • Gonorrhea • Skin disease • High/low BP • Migrane • Osteomyelitis • Contact with diagnosed or suspected Covid-19 patients • Diarrhoea	• GI endoscopy • APD • Leprosy • Epilepsy • Blood/Bleeding disorder • Tuberculosis • Polycythemia • G-6 PD deficiency • Fever • Travel outside country in the last 4 weeks	
4.	**During past 12 months have you had any of the following**		**Yes**	**No**
4.1	Received blood or blood components		Yes	No
4.2	Any accidents or operations?		Yes	No
4.3	Received any vaccinations?		Yes	No
4.4	Bitten by any animal, which can result in rabies?		Yes	No
4.5	Hand tattooing/ear piercing for acupuncture treatment?		Yes	No
4.6	Have you been imprisoned for any reasons?		Yes	No

Page No.: RLJH/C/BB-6

5.	**Have you had jaundice in the last 1 year?**	Yes	No
5.1	Has your blood ever tested positive for hepatitis B or C	Yes	No
5.2	Have you had close contact with anyone (family/others) suffering from jaundice in the last 1 year?	Yes	No
6.	**Have you had tuberculosis or tyohoid during the last year?**	Yes	No
7.	**Have you had malaria or taken antimalarial drugs in the last 3 years?**	Yes	No
8.	**Have you had any of the following in last 6 months?**	Yes	No
	Dental Procedure	Yes	No
	Measles	Yes	No
	Chicken Pox	Yes	No
	Dengue	Yes	No
9.	**Have you taken medicine in the last 7 days especially or antibiotics?**		
10.	**Do you know that you should not give blood in following conditions?**		
	If you were found to be HIV positive, Hepatitis B, C or Syphilis Infections	Yes	No
	If you are having multiple sex partners or have engaged in male to mal sexual activity	Yes	No
	If you have ever worked as a sex worker or had sex with a sex worker	Yes	No
	If you have ever injected any drug (esp. narcotics) not prescribed by a qualified doctor	Yes	No
	If you suspect that you or your partner may have HIV or any sexually transmitted disease	Yes	No
11.	**Do you or your sexual partner belonging to any of the above or below category**		
11.1	Do you have any reason to believe that you have been infected by the virus that can cause AIDS	Yes	No
11.2	In the last 6 months have you had.		
	Night Sweats	Yes	No
	Persistent Fever	Yes	No
	Unexplained Weight Loss	Yes	No
	Swollen Glands	Yes	No
	Persistent Diarrhea	Yes	No
12.	**In Case you are a women:**		
a	Are you pregnant or have you had an abortion in the last 6 months?	Yes	No
b	Do you have a child less than 1 year of age?	Yes	No
c	Are you Menstruating	Yes	No
d	Are you breast feeding?	Yes	No
13.	**Are you haveing minor non-specific symptoms including but not limited to general malaise, pain, headache**		

MEDICAL ASSESSMENT	Name of Medical Officer	Sign.:
Donor's Name: **Weight: Kgs, Hb Level: 12.5 g/dl - Yes / No, g/dl, BP - mm Hg,**		
History check list	Feeling well / adequate sleep (>5hrs)/Last meal within 4 hrs Every Hospitalized Current illness or medications:	
Examination Check list	Unhealthy look / pallor / icterus / alcohol smell infected wounds / Venipuncture site lesions	
Counseling Points	Post donation instruction / Making a regular donor Need for follow up for TTI purposes How to contact for follow up purposes By a letter / By phone / by e-mail	
Outcome	Donor accepted / Temporary deferral / Permanent deferral	
Remarks / Reasons for Deferral:		

REGISTRATION	Name of Medical Officer	Date:
Donors I.D. No.	Blood Group	Segment No.
Type of Bag:	**Single / Double / Triple / Quadruple**	
BLOOD COLLECTION	Name of Phlebotomist:	Signature
Check : Donor's Name Check Donation No: On Donation record / Blood Bags / Specimen Tubes Start time:..... a.m. / p.m. Time of Taken :..... Mins. Volume : ..... ml		
Complications : None : Faint: Fits: Double Prick: Hematoma: Others (Please specifY): Management:		

CONSENT

I understand that:

(a) Blood donation is a totally voluntary act and no inducement or remuneration has been offered.

(b) Donation of blood/components is a medical procedure and that by donating voluntarily, I accept the risk associated with this procedure.

(c) My donated blood, Blood and components such as red cells, platelets, plasma is issued to patients as well as other blood banks. Excess plasma recovered from my donated blood may be sent for plasma fractionation for preparation of plasma derived medicinal products, all of which may be used for large patient population and not just in this blood bank.

(d) My blood will be tested for Hepatitis B, Hepatitis C, Malaria Parasite, HIV/AIDS and Syphilis disease in addition to any other screening tests required ensuring blood safety.

(e) I would like to be informed about any abnormal test results done on my donated blood: Yes/No

(f) I, confirm that within 28 days from now, If I develop any symptoms of COVID-19 such as fever, Cough, Shortness of Breath, I Will inform the Blood Centre.

(g) I, hereby confirm that I did not have any symptoms of covid-19 in past one week.

Donor's Signature

Signature of Medical Officer

"BLOOD SAFETY BEGINS WITH A HEALTHY DONOR"

ಆರ್. ಎಲ್ ಜಾಲಪ್ಪ ಆಸ್ಪತ್ರೆ ಮತ್ತು ಸಂಶೋಧನಾ ಕೇಂದ್ರ ರಕ್ತ ನಿಧಿ

ತುಮಕ, ಕೋಲಾರ - 563 103.

Licence No.: KTK/28C-348/2018

ರಕ್ತದಾನಿಯ ನೋಂದಣಿ, ಪ್ರಶ್ನೆ ಮತ್ತು ಸಮ್ಮತಿ ಪ್ರತಿ

ರಕ್ತದಾನಿಗಳಾದ ನಿಮ್ಮ ಸುರಕ್ಷತೆಯನ್ನು ಮತ್ತು ನಿಮ್ಮ ರಕ್ತವನ್ನು ಸ್ವೀಕರಿಸುವ ರೋಗಿಗಳ ಸುರಕ್ಷತೆಯನ್ನು ಕಾಪಾಡಲು, ದಯವಿಟ್ಟು ಒದಗಿಸಿದ ಮಾಹಿತಿ ಕರಪತ್ರವನ್ನು ಓದಿ ಮತ್ತು ಈ ಪ್ರಶ್ನಾವಳಿಯನ್ನು ಸರಿಯಾಗಿ ಉತ್ತರಿಸಿ. ಈ ಫಾರ್ಮ್ ಅನ್ನು ಭರ್ತಿ ಮಾಡಲು ನಿಮಗೆ ಏನಾದರೂ ತೊಂದರೆ ಇದ್ದರೆ ದಯವಿಟ್ಟು ರಕ್ತ ಕೇಂದ್ರದ ಸಿಬ್ಬಂದಿಯಿಂದ ಸಹಾಯವನ್ನು ಕೇಳಿ, ನೀವು ನೀಡಿದ ಎಲ್ಲಾ ವಿವರಗಳನ್ನು ಗೌಪ್ಯವಾಗಿಡಲಾಗುತ್ತದೆ.

ದಾನಿಗಳ ಹೆಸರು:.....S/D/o..... ಆಧಾರ್ ಸಂಖ್ಯೆ:.....

ಹುಟ್ಟಿದ ದಿನಾಂಕ :..... ಲಿಂಗ : ಪುರುಷ / ಸ್ತ್ರಿ ವಯಸ್ಸು :..... ದೂರವಾಣಿ ಸಂಪರ್ಕ ಸಂಖ್ಯೆ:.....

ಇಮೇಲ್ :..... ಉದ್ಯೋಗ :.....

ವಿಳಾಸ:.....

ಸೂಕ್ತವಾದ ಕಡೆ ಟಿಕ್ ಮಾಡಿ (✓)

1.	ನೀವು ಈ ಹಿಂದೆ ರಕ್ತದಾನ ಮಾಡಿದ್ದೀರ?	ಹೌದು	ಇಲ್ಲ
1.1	ಹೌದು ಎಂದಾದರೆ ಎಷ್ಟು ಬಾರಿ	1.2 ಕೊನೆಯದಾಗಿ ದಾನ ಮಾಡಿದ ದಿನಾಂಕ :	
1.3	ಹಿಂದಿನ ದೇಣಿಗೆ ಸಮಯದಲ್ಲಿ ನೀವು ಯಾವುದೇ ಕಾಯಿಲೆ, ತೊಂದರೆ ಆಥವಾ ಅಸ್ವಸ್ಥತೆಯನ್ನು ಅನುಭವಿಸಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ
1.4	ಹೌದು ಎಂದಾದರೆ ತೊಂದರೆ ಎನು?		
1.5	ರಕ್ತದಾನ ಮಾಡದಂತೆ ನಿಮಗೆ ಎಂದಾದರೂ ಸಲಹೆ ನೀಡಲಾಗಿದೆಯೆ? ಹೌದು ಎಂದಾದರೆ ಏನು ಸಲಹೆ ನೀಡಲಾಗಿದೆ?	ಹೌದು	ಇಲ್ಲ
2.1	ನಿಮಗೆ ಇಂದು ಆರೋಗ್ಯವಾಗಿದೆಯೆ?	ಹೌದು	ಇಲ್ಲ
2.2	ಕಳೆದ 4 ಗಂಟೆಗಳಲ್ಲಿ ನೀವು ಏನನ್ನಾದರೂ ತಿಂದಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ
2.3	ರಕ್ತದಾನ ಮಾಡದ ನಂತರ ನೀವು ಭಾರೀ ಕೆಲಸದಲ್ಲಿ ತೊಡಗಬೇಕೇ/ಭಾರೀ ವಾಹನಗಳನ್ನು ಓಡಿಸಬೇಕೇ / ಎತ್ತರದಲ್ಲಿ ಕೆಲಸ ಮಾಡಬೇಕೇ?	ಹೌದು	ಇಲ್ಲ
3.	ನೀವು ಈ ಕೆಳಗಿನ ಯಾವುದಾದರು ರೋಗಲಕ್ಷಣಗಳನ್ನು ಹೊಂದಿದ್ದೀರಾ? ಹೌದು ಎಂದಾದರೆ ನೀವು ಇಲ್ಲಿರುವ ವೈದ್ಯರೊಂದಿಗೆ ಚರ್ಚಿಸಿ:		

• ಅಲರ್ಜಿ • ಕ್ಯಾನ್ಸರ್ • ಮೂರ್ಛೆ ಹೋಗುವ ರೋಗ • ಹೃದಯರೋಗ • ಶ್ವಾಸಕೋಶದ ಖಾಯಿಲೆ • ಉಬ್ಬಸ • ಥೈರಾಯ್ಡ್ ಖಾಯಿಲೆ • ಲೀಶ್ಮಾನಿಯಾಸಿಸ್ • ಅಟೋಇಮ್ಯೂನ್ ಖಾಯಿಲೆ • ಅಪಾಯದ ವರ್ತನೆ • ಮೂತ್ರಪಿಂಡ ಖಾಯಿಲೆ • ಉಸಿರಾಟದ ತೊಂದರೆ	• ಮಾನಸಿಕ ಅಸ್ವಸ್ಥತೆ/ಸ್ಕಿಜೋ ಫ್ರೇನಿಯಾ • ಅಮೀಬಿಯಾಸಿನ್ • ಶೀತ/ಕೆಮ್ಮು/ನೋಯುತ್ತಿರುವ ಗಂಟಲು/ತೀವ್ರವಾದ ಸೈನುಟಿಸ್ • ಹಿತ್ತಜನಕಾಂಗ ರೋಗ • ಹಿಮೋಗ್ಲೋಬಿನೋಪಥಿಸ್ • ಕೋವಿಡ್-19 ರೋಗ ಸಂಪರ್ಕ • 4 ವಾರಗಳಲ್ಲಿ ದೇಶದ ಹೊರಗೆ ಪ್ರಯಾಣ ಮಾಡಿರುವಿರಾ?	• ಅಂಗ, ಕಾಂಡಕೋಶ ಮತ್ತು ಅಂಗಾಂಶ ಕಸಿ ಸ್ವೀಕರಿಸುವುದು • ನಿರ್ನಾಳಗ್ರಂಥಿ ಖಾಯಿಲೆ • ಮಧುಮೇಹ • ಸಿಫಿಲಿಸ್ • ಗೊನೊರಿಯಾ • ಚರ್ಮದ ಕಾಯಿಲೆ • ಬಿಪಿಯಲ್ಲಿ ಏರು ಪೇರು • ಮೈಗ್ರೇನ್ • ಆಸ್ಟಿಯೋಮೈಲಿಟಿಸ್	• ಇತರ ದೇಶಗಳ ನಿವಾಸಿಗಳು • ಅತಿಸಾರ • ಜಿಐ ಎಂಡೋಸ್ಕೋಪಿ • ಎಪಿಡಿ • ಕುಷ್ಠರೋಗ • ಮಲರೋಗ • ರಕ್ತ/ರಕ್ತಸ್ರಾವದ ಕಾಯಿಲೆ • ಕ್ಷಯ • ಪಾಲಿಸಿಥೆಮಿಯಾ • ಜಿ-6 ಪಿಡಿ ಕೋರತೆ • ಜ್ವರ

4.	ಕಳೆದ 12 ತಿಂಗಳುಗಳಲ್ಲಿ ನೀವು ಈ ಕೆಳಗಿನ ಯಾವುದನ್ನಾದರೂ ಹೊಂದಿದ್ದೀರಾ	ಹೌದು	ಇಲ್ಲ
41	ರಕ್ತ ಅಥವಾ ರಕ್ತದ ಘಟಕಗಳ ನೀವು ಸ್ವೀಕರಿಸಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ
4.2	ಯಾವುದೇ ಅಪಘಾತಗಳು ಅಥವಾ ಶಸ್ತ್ರಚಿಕಿತ್ಸೆ ಆಗಿದೆಯೆ?	ಹೌದು	ಇಲ್ಲ
4.3	ಯಾವುದೇ ವಾಕ್ಸಿನೇಷನ್ ಸ್ವೀಕರಿಸಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ
4.4	ರೆಬೀಸ್ ಕಾಯಿಲೆ ಬರುವಂತಹ ಯಾವುದೇ ಪ್ರಾಣಿ ಕಚ್ಚಿದೆಯಾ?	ಹೌದು	ಇಲ್ಲ
4.5	ಕೈ ಹಚ್ಚೆ / ಅಕ್ಯುಪಂಕ್ಚರ್ ಚಿಕಿತ್ಸೆಗಾಗಿ ಕಿವಿ ಚುಚ್ಚುಸಿಕೊಂಡಿದ್ದಿರಾ?	ಹೌದು	ಇಲ್ಲ
4.6	ಯಾವುದೇ ಕಾರಣಗಳಿಗಾಗಿ ನೀವು ಜೈಲಿನಲ್ಲಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ

5.	ಕಳೆದ 1 ವರ್ಷದಲ್ಲಿ ಕಾಮಾಲೆ ಹೊಂದಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ
5.1	ಎಂದಾದರು ನಿಮ್ಮ ರಕ್ತವು ಹೆಪಟೈಟಿಸ್ ಬಿ ಅಥವಾ ಸಿ ಪೊಸಿಟೀವ್ ಆಗಿರುವುದಾ?	ಹೌದು	ಇಲ್ಲ
5.2	ಕಳೆದ 1 ವರ್ಷದಲ್ಲಿ ಕಾಮಾಲೆ ರೋದಿಂದ ಬಳಲುತ್ತಿರುವ ಯಾವುದಾದರು ರೋಗಿಯ ಜೊತೆ (ಕುಟುಂಬ / ಇತರರು) ನೀವು ನಿಕಟ ಸಂಪರ್ಕ ಹೊಂದಿದೀರಾ?	ಹೌದು	ಇಲ್ಲ
6.	ಕಳೆದ ವರ್ಷದಲ್ಲಿ ನೀವು ಕ್ವಯ ಅಥವಾ ಟೈಪಾಯಿಡ್ ಹೊಂದಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ
7.	ಕಳೆದ 3 ವರ್ಷದಲ್ಲಿ ನೀವು ಮಲೇರಿಯಾವನ್ನು ಹೊಂದಿದ್ದೀರಾ ಅಥವಾ ಅಂಟಿಮಾಲೇರಿಯಲ್ ಔಷಧಿಗಳನ್ನು ತೆಗೆದುಕೊಂಡಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ
8.	ಕಳೆದ 6 ತಿಂಗಳಲ್ಲಿ ನೀವು ಈ ಕೆಳಗಿನವುಗಳನ್ನು ಹೊಂದಿದ್ದೀರಾ?		
	ದಂತ ಚಿಕಿತ್ಸೆ	ಹೌದು	ಇಲ್ಲ
	ದಡಾರ	ಹೌದು	ಇಲ್ಲ
	ಚಿಕನ್ ಪೋಕ್ಸ್	ಹೌದು	ಇಲ್ಲ
	ಡೆಂಗ್ಯೂ	ಹೌದು	ಇಲ್ಲ
9.	ಕಳೆದ 7 ದಿನಗಳಲ್ಲಿ ನೀವು ಅಂಟಿಬಯೊಟಿಕ್ ಅಥವಾ ಬೇರೆ ಪ್ರತಿಜೀವಕಗಳನ್ನು ಸೇವಿಸಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ
10.	ಈ ಕೆಳಗಿನ ಪರಿಸ್ಥಿತಿಗಳಲ್ಲಿ ನೀವು ರಕ್ತವನ್ನು ನೀಡಬಾರದು ಎಂದು ನಿಮಗೆ ತಿಳಿದಿದೇಯೇ?		
	ನೀವು ಹೆಚ್.ಐ.ವಿ. ಪಾಸಿಟಿವ್, ಹೆಪಟೈಟಿಸ್ ಬಿ.ಸಿ. ಅಥವಾ ಸಿಫಿಲಿಸ್ ಸೋಂಕು ಪೊಸಿಥಟಿವ್	ಹೌದು	ಇಲ್ಲ
	ನೀವು ಅನೇಕ ಲೈಂಗಿಕ ಸಂಪರ್ಕ ಹೊಂದಿದ್ದರೆ ಅಥವಾ ಪುರುಷರಿಂದ ಪುರುಷ ಲೈಂಗಿಕ ಚಟುವಟಿಕೆಯಲ್ಲಿ ತೊಡಗಿದ್ದರೆ	ಹೌದು	ಇಲ್ಲ
	ನೀವು ಎಂದಾದರೂ ಲೈಂಗಿಕ ಕಾರ್ಯಕರ್ತೆಯಾಗಿ ಕಲಸ ಮಾಡಿದ್ದರೆ ಅಥವಾ ಲೈಂಗಿಕ ಕಾರ್ಯಕರ್ತೆಯೊಂದಿಗೆ ಲೈಂಗಿಕ ಸಂಬಂಧ ಹೊಂದಿದ್ದರೆ	ಹೌದು	ಇಲ್ಲ
	ಅರ್ಹ ವೈದ್ಯರಿಂದ ಶಿಫಾರಸು ಮಾಡದ ಯಾವುದೇ ಔಷಧಿಯನ್ನು (ಮಾದಕವಸ್ತು) ನೀವು ಎಂದಾದರೂ ಇಂಜೆಕ್ಟ್ ಮಾಡಿಕೊಂಡಿದ್ದರೆ ತಿಳಿಸಿ?	ಹೌದು	ಇಲ್ಲ
	ನೀವು ಅಥವಾ ನಿಮ್ಮ ಸಂಗಾತಿ ಎಚ್.ಐ.ವಿ. ಅಥವಾ ಯಾವುದೇ ಲೈಂಗಿಕವಾಗಿ ಹರಡುವ ರೋಗವನ್ನು ಹೊಂದಿರಬಹುದು ಎಂದು ನೀವು ಅನುಮಾನಿಸಿದರೆ?	ಹೌದು	ಇಲ್ಲ
11.	ನೀವು ಅಥವಾ ನಿಮ್ಮ ಲೈಂಗಿಕ ಸಂಗಾತಿ ಮೇಲಿನ ಅಥವಾ ಕೆಳಗಿನ ಯಾವುದೇ ವರ್ಗಕ್ಕೆ ಸೇರಿದವರೇ?	ಹೌದು	ಇಲ್ಲ
11.1	ಐಡ್ಸ್‌ಗೆ ಕಾರಣವಾಗುವ ವೈರಸ್‌ನಿಂದ ನೀವು ಸೋಂಕಿಗೆ ಒಳಗಾಗಿದ್ದೀರಿ ಎಂದು ನಂಬಲು ನೀಮಗೆ ಯಾವುದೇ ಕಾರಣವಿದೆಯೇ?	ಹೌದು	ಇಲ್ಲ
11.2	ಕಳೆದ 6 ತಿಂಗಳಲ್ಲಿ ನೀವು ಈ ಯಾವುದಾದರಿಂದ ಬಳಲಿದ್ದೀರ:		
	ರಾತ್ರಿ ಬೆವರು	ಹೌದು	ಇಲ್ಲ
	ನಿರಂತರ ಜ್ವರ	ಹೌದು	ಇಲ್ಲ
	ವಿವರಿಸಲಾಗದ ತೂಕ ನಷ್ಟ	ಹೌದು	ಇಲ್ಲ
	ಊದಿಕೊಂಡ ಗ್ರಂಥಿಗಳು	ಹೌದು	ಇಲ್ಲ
	ನಿರಂತರ ಅತಿಸಾರ	ಹೌದು	ಇಲ್ಲ
12.	ನೀವು ಮಹಿಳೆಯಾಗಿದ್ದರೆ	ಹೌದು	ಇಲ್ಲ
ಎ.	ನೀವು ಗರ್ಭಿಣಿಯಾಗಿದ್ದೀರಾ ಅಥವಾ ಕಳೆದ 6 ತಿಂಗಳಲ್ಲಿ ನೀಮಗೆ ಗರ್ಭಪಾತ ಆಗಿದೆಯಾ?	ಹೌದು	ಇಲ್ಲ
ಬಿ.	ನೀವು 1 ವರ್ಷಕ್ಕಿಂತ ಕಡಿಮೆ ವಯಸ್ಸಿನ ಮಗುವನ್ನು ಹೊಂದಿದ್ದೀರಾ? ನೀವು ಸ್ತನ್ಯಪಾನ ಮಾಡುತಿದಿರಾ?	ಹೌದು	ಇಲ್ಲ
ಸಿ.	ನೀವು ಮುಟ್ಟಾಗಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ
13.	ನೀವು ಸಣ್ಣ ಪ್ರಮಾಣದ ಯಾವುದೆ ಅಸ್ವಸ್ತತೆ, ತಲೆನೋವು ಸೇರಿದಂತೆ ಸಣ್ಣ ರೋಗಲಕ್ಷಣಗಳನ್ನು ಹೊಂದಿದ್ದೀರಾ?	ಹೌದು	ಇಲ್ಲ

ಒಪ್ಪಿಗೆ

ನಾನು ಇದನ್ನು ಅರ್ಥಮಾಡಿಕೊಂಡಿದ್ದೇನೆ:

ಎ. ರಕ್ತದಾನವು ಸಂಪೂರ್ಣವಾಗಿ ಸ್ವಯಂಪ್ರೇರಿತ ಕಾರ್ಯವಾಗಿದೆ ಮತ್ತು ಯಾವುದೇ ಪ್ರಚೋದನೆ ಅಥವಾ ಸಂಭಾವನೆಯನ್ನು ನೀಡಲಾಗುವುದಿಲ್ಲ

ಬಿ. ರಕ್ತ / ರಕ್ತ ಘಟಕಗಳ ದಾನವು ವೈದ್ಯಕೀಯ ವಿಧಾನವಾಗಿದೆ ಮತ್ತು ಸ್ವಯಂಪ್ರೇರಣೆಯಿಂದ ದಾನ ಮಾಡುತ್ತಿರುವೆನು, ಈ ಕಾರ್ಯವಿಧಾನಕ್ಕೆ ಸಂಬಂಧಿಸಿದ ಅಪಾಯವನ್ನು ನಾನು ಸ್ವೀಕರಿಸುತ್ತೇನೆ.

ಸಿ. ದಾನ ಮಾಡಿದ ನನ್ನ ರಕ್ತ. ಕೆಂಪು ಕೋಶಗಳು, ಪ್ಲೇಟ್‌ಲೆಟ್‌ಗಳು, ಪ್ಲಾಸ್ಮಾ ಮುಂತಾದ ಘಟಕಗಳನ್ನು ರೋಗಿಗಳಿಗೆ ಮತ್ತು ಇತರ ರಕ್ತ ಬ್ಯಾಂಕ್ ಗಳಿಗೆ ನೀಡಲಾಗುತ್ತದೆ. ನಾನು ದಾನ ಮಾಡಿದ ರಕ್ತದಿಂದ ಬೇರ್ಪಡಿಸಲಾಗದ ಹೆಚ್ಚುವರಿ ಪ್ಲಾಸ್ಮಾವನ್ನು ವಿಭಾಗೀಕರಣ ಕಳುಹಿಸಬಹುದು ಮತ್ತು ಅದರಿಂದ ಔಷಧೀಯ ಉತ್ಪನ್ನಗಳನ್ನು ತಯಾರಿಸಲಾಗುವುದು. ಇವೆಲ್ಲವನ್ನೂ ಈ ರಕ್ತದ ಬ್ಯಾಂಕಿನಲ್ಲಿ ಮಾತ್ರವಲ್ಲದೆ ಅನ್ಯ ರೋಗಿಗಳಿಗೆ ಬಳಸಬಹುದು.

ಡಿ. ನನ್ನ ರಕ್ತವನ್ನು ಹೆಪಟೈಟಿಸ್ ಬಿ. ಹೆಪಟೈಟಿಸ್ ಸಿ. ಮಲೇರಿಯಾ. ಹೆಚ್.ಐ.ವಿ. / ಐಡ್ಸ್ ಮತ್ತು ಸಿಫಿಲಿಸ್ ಕಾಯಿಲೆಗೆ ಪರೀಕ್ಷಿಸಲಾಗುವುದು ಮತ್ತು ರಕ್ತದ ಸುರಕ್ಷತೆಯನ್ನು ಖಾತರಿಪಡಿಸುವ ಅಗತ್ಯವಿರುವ ಪರೀಕ್ಷೆಗಳನ್ನು ಮಾಡಲಾಗುವುದು. ಜೊತೆಗೆ

ಇ. ನಾನು ದಾನ ಮಾಡಿದ ರಕ್ತದ ಮೇಲೆ ಮಾಡಿದ ಯಾವುದೇ ಅಸಹಜ ಪರೀಕ್ಷಾ ಫಲಿತಾಂಶಗಳ ಬಗ್ಗೆ ನನಗೆ ತಿಳಿಸಲು ಬಯಸುತ್ತೇನೆ: ಹೌದು / ಇಲ್ಲ

ಎಫ್. ನಾನು ಇಂದಿನಿಂದ 28 ದಿನಗಳಲ್ಲಿ ಜ್ವರ, ಕೆಮ್ಮು, ಉಸಿರಾಟದ ತೊಂದರೆ ಮುಂತಾದ ಕೋವಿಡ್-19 ಯಾವುದೇ ರೋಗಲಕ್ಷಣಗಳನ್ನು ಕಂಡರೆ ರಕ್ತ ಕೇಂದ್ರಕ್ಕೆ ತಿಳಿಸುತ್ತೇನೆ.

ದಾನಿಗಳ ಸಹಿ

ವೈದ್ಯಕೀಯ ಅಧಿಕಾರಿಯ ಸಹಿ

''ಸುರಕ್ಷತೆಯು ಆರೋಗ್ಯಕರ ದಾನಿಯೊಂದಿಗೆ ಪ್ರಾರಂಭವಾಗುತ್ತದೆ''

SDUAHER

SRI DEVARAJ URS ACADEMY OF HIGHER EDUCATION & RESEARCH

SRI DEVARAJ URS MEDICAL COLLEGE

Tamaka, Kolar

INSTITUTIONAL ETHICS COMMITTEE

No. DMC/KLR/UDOME/IEC/ 15 / 2012-13 Date:09-03-2012

From,

The Institutional Ethical Committee,
Sri Devaraj Urs Medical College,
Tamaka, Kolar-563101

To,

Dr. Subhashis Das
Ph.D. Scholar,
Department of Pathology,
Sri Devaraj Urs Medical College,
Tamaka, Kolar-563101

Subject: Comments on the paper.

This is to certify that the institutional ethics committee of Sri Devaraj Urs Medical College, Tamaka, Kolar has examined and unanimously approved the Ph.D. topic "Extension of The Shelf Life of Platelets; Prospects and Pitfalls" of Dr. Subhashis Das, Ph.D. Scholar in the Department of Pathology under the guidance of Dr. Harendra Kumar M L, Professor & HOD of Pathology at SDUMC, Kolar.

Member Secretary
Member Secretary
Ethical Committee
SDUMC, Kolar.

Principal
Principal
Sri Devaraj Urs Medical College
Tamaka, Kolar-563101.

Original Article

Quality Implications of Regular Versus Overnight Processing of Stored Human Platelets: An Institutional Study

Subhashish Das, Harendra Kumar M L

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ABSTRACT

Background: Platelet concentrates (PC) are prepared from random donor platelets (RDP) and single donor platelets (SDP) and the various quality parameters of the PC are multifactorial which includes the preparation techniques, types of bags used, holding period prior to processing, type of anticoagulant used, use of additive solutions, the storage conditions after processing, etc. Extending the holding period before processing and ensuring the absence of deleterious affect on the quality parameters of the PC can be extremely beneficial from operational and logistical reasons to meet the increased clinical demand of PCs, particularly for oncology cases and during dengue epidemic. Aims and Objectives: The comparative evaluation of various quality parameters including morphological, biochemical and molecular aspects of PCs between fresh whole blood (WB) (8 hrs) versus overnight hold blood (24 hrs) on the 0, 3rd and 5th day of storage. **Materials and Methods:** Fifty units of blood were collected and stored overnight (24 hrs) hours at a temperature of 22°C to 24°C and processed subsequently. The other 50 units were processed immediately within 8 hours. All the PCs had undergone mandatory serological testing and all the sero-negative PCs had fulfilled quality control parameters. Sterility confirmation was done on 0, 3rd and 5th day of storage. Morphological, biochemical and molecular aspects for both the categories of PCs were studied. For statistical analysis, *t*-test at 95% confidence interval was done with a *P* value of <0.05 taken as statistically significant. **Results:** All essential quality parameters in both the categories of PCs were within acceptable limits. No adverse impact on quality was noted in the overnight PCs. **Conclusion:** The preserved quality of overnight PCs along with associated logistic benefits should encourage blood bank management to seriously explore the feasibility of undertaking the 24-hours whole blood holding period (overnight) before preparing PCs.

KEYWORDS: *Fresh, overnight, platelet concentrates, quality parameters*

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INTRODUCTION

Platelet transfusion is usually different from various other routine blood transfusion because of certain unique features including the limited shelf life, bacterial contamination and its various mode of collection, preparation and storage. This is because structural characteristics of the platelets along with their biochemical features directly affect the platelet functional qualities and consequently the clinical outcome.[1]

Of all the blood components, platelet inventory management remains a challenge because of the demand–supply scenario. Platelet inventory management is characterized by a limited shelf life and a limited donor base and restricted number of blood donations,

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Original Article

Comparative Evaluation of Quality Parameters of Platelet Stored in Additive Solution versus Plasma

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Abstract

Introduction: Extension of the shelf life of platelets remains a challenge for transfusion services, and efforts techniques are required to extend the shelf life of platelets beyond 5 days without compromising their qualities. **Materials and Methods:** The study is being done to compare *in vitro* changes of platelet indices-platelet count, mean platelet volume, platelet distribution width (PDW), pH and swirling in stored platelet concentrate (PC) with and without platelet additive solution (PAS) for 0,3,5,7 and 10 days. **Results:** Serial measurements of various parameters in PCs with and without PAS showed that PCs stored in PAS were better maintained and had optimal quality standards throughout the extended storage time as compared to the PCs without PAS. The results obtained in both categories were statistically significant ($P < 0.001$). **Conclusion:** Our study showed that the use of PAS in the PCs increased the shelf life and improved the viability of platelets as compared to the PCs without PAS.

Keywords: Additive solution, plasma, platelet concentrate

Introduction

Platelets were first identified in the year 1881,[1] and the first effort to increase the platelet counts in cases of thrombocytopenia by transfusion of whole blood was described by Duke in the year 1910.[1] General improvement of the technique to separate platelets from whole blood and availability of plastic bags in blood banking revolutionised the field of components therapy.

During the storage period, the platelet concentrate (PC) undergoes biochemical, structural and functional changes, which is collectively termed as platelet storage lesion (PSL)[2] and has a negative impact on the post-transfusion increment. Platelet indices such as the platelet count, mean platelet volume (MPV), PDW and PC are considered as representative of storage-induced shape changes in PC along with the swirling test.[3] Swirling test is used for detecting variation in shape, and its absence is highly predictive of poor post-transfusion PC increments.[4]

The occurrence of PSL is multifactorial, including the methods of collection, processing, storage and transportation after collection can result in PSL. These lesions are associated with decreased *in vivo* platelet recovery, survival and haemostatic activity after transfusion.[5]

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Aims and objectives

The present study was carried out to assess the changes in some of the *in vitro* parameters of PC stored for 10 days with and without platelet additive solutions (PASs).

The aims and objective of the study were:

1. To study and compare the various morphological parameters of platelets with and without PAS on days 0, 3,5,7 and 10
2. To study and compare the pH values and sterility of platelets with and without PAS on days 0, 3,5,7 and 10.

Materials and Methods

The study sample included 130 voluntary blood donors who were selected as per the director general of health services criteria.[6] Pre-donation counselling and a medical examination

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MASTER CHARTS

	WITH PAS - DAY 0 1(a)										
Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
1	1	Human_Uniprot_2018	sp|P02768|ALBU_HUMAN	8323	71317	358	358	28	28	5.78	Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2
2	1	Human_Uniprot_2018	sp|P01024|CO3_HUMAN	3859	188569	140	140	45	45	2.08	Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2
3	1	Human_Uniprot_2018	sp|P01023|A2MG_HUMAN	3046	164613	119	119	36	36	1.8	Alpha-2-macroglobulin OS=Homo sapiens OX=9606 GN=A2M PE=1 SV=3
4	1	Human_Uniprot_2018	sp|P04114|APOB_HUMAN	2833	516651	131	131	81	81	1.1	Apolipoprotein B-100 OS=Homo sapiens OX=9606 GN=APOB PE=1 SV=2
5	1	Human_Uniprot_2018	sp|P02787|TRFE_HUMAN	2730	79294	112	112	17	17	2.09	Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=3
6	1	Human_Uniprot_2018	sp|P01834|IGKC_HUMAN	2377	11929	94	94	6	6	9.3	Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2
7	1	Human_Uniprot_2018	sp|P01009|A1AT_HUMAN	2168	46878	81	81	18	18	5.08	Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3
8	1	Human_Uniprot_2018	sp|P02647|APOA1_HUMAN	2080	30759	72	72	25	25	43.97	Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1
9	1	Human_Uniprot_2018	sp|P02675|FIBB_HUMAN	1898	56577	73	73	19	19	3.84	Fibrinogen beta chain OS=Homo sapiens OX=9606 GN=FGB PE=1 SV=2
10	1	Human_Uniprot_2018	tr|A0A0A0MS08|A0A0A0MS08_HUMAN	1810	44511	64	64	7	7	1.09	Immunoglobulin heavy constant gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1
10	2	Human_Uniprot_2018	sp|P01861|IGHG4_HUMAN	910	36431	28	28	6	6	1.17	Immunoglobulin heavy constant gamma 4 OS=Homo sapiens OX=9606 GN=IGHG4 PE=1 SV=1
10	3	Human_Uniprot_2018	sp|P01859|IGHG2_HUMAN	645	36505	32	32	5	5	1.16	Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=2
10	4	Human_Uniprot_2018	sp|P01860|IGHG3_HUMAN	622	42287	30	30	5	5	0.74	Immunoglobulin heavy constant gamma 3 OS=Homo sapiens OX=9606 GN=IGHG3 PE=1 SV=2
11	1	Human_Uniprot_2018	sp|P0C0L5|CO4B_HUMAN	1677	194170	61	61	31	31	1.12	Complement C4-B OS=Homo sapiens OX=9606 GN=C4B PE=1 SV=2
11	2	Human_Uniprot_2018	tr|A0A0G2JL54|A0A0G2JL54_HUMAN	1661	189080	60	60	31	31	1.17	Complement C4-B OS=Homo sapiens OX=9606 GN=C4B_2 PE=1 SV=1
11	3	Human_Uniprot_2018	sp|P0C0L4|CO4A_HUMAN	1367	194261	53	53	30	30	1.07	Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=2
12	1	Human_Uniprot_2018	sp|P02766|TTHY_HUMAN	1455	15991	51	51	10	10	17.26	Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1
13	1	Human_Uniprot_2018	sp|P02671-2|FIBA_HUMAN	1324	70227	54	54	11	11	1.23	Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA
14	1	Human_Uniprot_2018	sp|P00450|CERU_HUMAN	992	122983	46	46	20	20	1.15	Ceruloplasmin OS=Homo sapiens OX=9606 GN=CP PE=1 SV=1
14	2	Human_Uniprot_2018	tr|E9PFZ2|E9PFZ2_HUMAN	772	109493	40	40	19	19	1.27	Ceruloplasmin OS=Homo sapiens OX=9606 GN=CP PE=1 SV=1
15	1	Human_Uniprot_2018	sp|P02751-14|FINC_HUMAN	863	252838	36	36	21	21	0.48	Isoform 14 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1
16	1	Human_Uniprot_2018	tr|B7ZKJ8|B7ZKJ8_HUMAN	826	104044	36	36	18	18	1.26	ITIH4 protein OS=Homo sapiens OX=9606 GN=ITIH4 PE=1 SV=1
17	1	Human_Uniprot_2018	tr|A0A1B0GUU9|A0A1B0GUU9_HUMAN	760	52518	34	34	8	8	1.05	Immunoglobulin heavy constant mu (Fragment) OS=Homo sapiens OX=9606 GN=IGHM PE=1 SV=1
18	1	Human_Uniprot_2018	sp|P01011|AACT_HUMAN	748	47792	21	21	11	11	1.94	Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=2
19	1	Human_Uniprot_2018	sp|A0M8Q6|IGLC7_HUMAN	697	11418	26	26	3	3	2.35	Immunoglobulin lambda constant 7 OS=Homo sapiens OX=9606 GN=IGLC7 PE=1 SV=3
19	2	Human_Uniprot_2018	sp|B9A064|IGLL5_HUMAN	538	23391	22	22	3	3	0.82	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens OX=9606 GN=IGLL5 PE=2 SV=2
20	1	Human_Uniprot_2018	tr|A0A286YEY1|A0A286YEY1_HUMAN	680	43620	20	20	3	3	0.38	Immunoglobulin heavy constant alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=1
20	2	Human_Uniprot_2018	tr|A0A0G2JMB2|A0A0G2JMB2_HUMAN	563	37283	17	17	3	3	0.46	Immunoglobulin heavy constant alpha 2 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA2 PE=1 SV=1
21	1	Human_Uniprot_2018	sp|P01008|ANT3_HUMAN	668	53025	35	35	13	13	2.16	Antithrombin-III OS=Homo sapiens OX=9606 GN=SERPINC1 PE=1 SV=1
22	1	Human_Uniprot_2018	sp|P01619|KV320_HUMAN	636	12663	10	10	3	3	1.99	Immunoglobulin kappa variable 3-20 OS=Homo sapiens OX=9606 GN=IGKV3-20 PE=1 SV=2
23	1	Human_Uniprot_2018	tr|C9JC84|C9JC84_HUMAN	631	52932	27	27	9	9	1.22	Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=1
24	1	Human_Uniprot_2018	sp|P19827|ITIH1_HUMAN	562	101782	19	19	10	10	0.59	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens OX=9606 GN=ITIH1 PE=1 SV=3
25	1	Human_Uniprot_2018	tr|A0A2R8Y793|A0A2R8Y793_HUMAN	530	34405	21	21	8	8	1.97	Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1
25	2	Human_Uniprot_2018	sp|P68032|ACTC_HUMAN	226	42334	12	12	5	5	0.74	Actin, alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1
26	1	Human_Uniprot_2018	tr|Q5T985|Q5T985_HUMAN	493	105606	26	26	13	13	0.79	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens OX=9606 GN=ITIH2 PE=1 SV=1
27	1	Human_Uniprot_2018	sp|P02790|HEMO_HUMAN	474	52385	25	25	8	8	1.05	Hemopexin OS=Homo sapiens OX=9606 GN=HPX PE=1 SV=2
28	1	Human_Uniprot_2018	tr|D6RF35|D6RF35_HUMAN	471	54583	18	18	6	6	0.68	Vitamin D-binding protein OS=Homo sapiens OX=9606 GN=GC PE=1 SV=1
29	1	Human_Uniprot_2018	sp|P04196|HRG_HUMAN	431	60510	15	15	5	5	0.47	Histidine-rich glycoprotein OS=Homo sapiens OX=9606 GN=HRG PE=1 SV=1
30	1	Human_Uniprot_2018	sp|P04264|K2C1_HUMAN	416	66170	17	17	9	9	0.9	Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6
30	2	Human_Uniprot_2018	sp|P35908|K22E_HUMAN	124	65678	3	3	3	3	0.24	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2
31	1	Human_Uniprot_2018	sp|P02763|A1AG1_HUMAN	410	23725	21	21	5	5	1.67	Alpha-1-acid glycoprotein 1 OS=Homo sapiens OX=9606 GN=ORM1 PE=1 SV=1
31	2	Human_Uniprot_2018	sp|P19652|A1AG2_HUMAN	155	23873	9	9	3	3	0.8	Alpha-1-acid glycoprotein 2 OS=Homo sapiens OX=9606 GN=ORM2 PE=1 SV=2
32	1	Human_Uniprot_2018	tr|A0A2Q2TTZ9|A0A2Q2TTZ9_HUMAN	401	11949	6	6	2	2	1.16	Immunoglobulin kappa variable 1-33 OS=Homo sapiens OX=9606 GN=IGKV1D-33 PE=1 SV=1
33	1	Human_Uniprot_2018	sp|P68871|HBB_HUMAN	394	16102	14	14	6	6	4.65	Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2
34	1	Human_Uniprot_2018	sp|P06396|GELS_HUMAN	376	86043	13	13	8	8	0.55	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
35	1	Human_Uniprot_2018	sp|P04217|A1BG_HUMAN	348	54790	16	16	7	7	0.82	Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=4
36	1	Human_Uniprot_2018	sp|P05155-2|IC1_HUMAN	346	49954	13	13	8	8	1.12	Isoform 2 of Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1
37	1	Human_Uniprot_2018	sp|P06727|APOA4_HUMAN	328	45371	16	16	8	8	1.29	Apolipoprotein A-IV OS=Homo sapiens OX=9606 GN=APOA4 PE=1 SV=3
38	1	Human_Uniprot_2018	tr|J3QLC9|J3QLC9_HUMAN	325	41381	14	14	5	5	0.76	Haptoglobin (Fragment) OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1
39	1	Human_Uniprot_2018	sp|P02649|APOE_HUMAN	325	36246	13	13	6	6	1.17	Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1
40	1	Human_Uniprot_2018	tr|E9PIT3|E9PIT3_HUMAN	324	66792	12	12	4	4	0.33	Prothrombin OS=Homo sapiens OX=9606 GN=F2 PE=1 SV=1
41	1	Human_Uniprot_2018	sp|P01019|ANGT_HUMAN	272	53406	11	11	5	5	0.55	Angiotensinogen OS=Homo sapiens OX=9606 GN=AGT PE=1 SV=1
42	1	Human_Uniprot_2018	tr|A0A0B4J2B5|A0A0B4J2B5_HUMAN	264	10764	9	9	2	2	1.35	Immunoglobulin heavy variable 3/OR16-9 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV3OR16-9 PE=1 SV=1
43	1	Human_Uniprot_2018	sp|P10909-2|CLUS_HUMAN	244	58537	10	10	5	5	0.49	Isoform 2 of Clusterin OS=Homo sapiens OX=9606 GN=CLU
44	1	Human_Uniprot_2018	sp|P25311|ZA2G_HUMAN	242	34465	11	11	6	6	1.26	Zinc-alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=AZGP1 PE=1 SV=2
45	1	Human_Uniprot_2018	sp|P08603|CFAH_HUMAN	240	143680	13	13	6	6	0.22	Complement factor H OS=Homo sapiens OX=9606 GN=CFH PE=1 SV=4
46	1	Human_Uniprot_2018	sp|P04004|VTNC_HUMAN	239	55069	11	11	3	3	0.29	Vitronectin OS=Homo sapiens OX=9606 GN=VTN PE=1 SV=1

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
47	1	Human_Uniprot_2018	tr|B0YIW2|B0YIW2_HUMAN	230	12864	6	6	2	2	1.05	Apolipoprotein C-III variant 1 OS=Homo sapiens OX=9606 GN=APOC3 PE=1 SV=1
48	1	Human_Uniprot_2018	tr|C9JV77|C9JV77_HUMAN	216	40185	5	5	1	1	0.26	Alpha-2-HS-glycoprotein OS=Homo sapiens OX=9606 GN=AHSG PE=1 SV=1
49	1	Human_Uniprot_2018	sp|P13645|K1C10_HUMAN	214	59020	11	11	7	7	0.75	Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6
50	1	Human_Uniprot_2018	sp|P01042-2|KNG1_HUMAN	200	48936	8	8	4	4	0.47	Isoform LMW of Kininogen-1 OS=Homo sapiens OX=9606 GN=KNG1
51	1	Human_Uniprot_2018	tr|A0A0G2JPA8|A0A0G2JPA8_HUMAN	186	48135	9	9	5	5	0.63	Alpha-2-antiplasmin OS=Homo sapiens OX=9606 GN=SERPINF2 PE=1 SV=1
52	1	Human_Uniprot_2018	sp|Q9Y490|TLN1_HUMAN	184	271766	12	12	11	11	0.21	Talin-1 OS=Homo sapiens OX=9606 GN=TLN1 PE=1 SV=3
53	1	Human_Uniprot_2018	sp|P01597|KV139_HUMAN	169	12900	6	6	2	2	1.05	Immunoglobulin kappa variable 1-39 OS=Homo sapiens OX=9606 GN=IGKV1-39 PE=1 SV=2
54	1	Human_Uniprot_2018	tr|A0A024R0T9|A0A024R0T9_HUMAN	166	11277	7	7	3	3	2.39	Apolipoprotein C-II isoform 1 OS=Homo sapiens OX=9606 GN=APOC4-APOC2 PE=1 SV=1
55	1	Human_Uniprot_2018	sp|P02775|CXCL7_HUMAN	161	14171	6	6	2	2	0.92	Platelet basic protein OS=Homo sapiens OX=9606 GN=PPBP PE=1 SV=3
56	1	Human_Uniprot_2018	tr|V9GYE3|V9GYE3_HUMAN	148	5873	6	6	2	2	3.63	Apolipoprotein A-II OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1
57	1	Human_Uniprot_2018	tr|A0A0A0MSV6|A0A0A0MSV6_HUMAN	147	24243	5	5	3	3	0.78	Complement C1q subcomponent subunit B (Fragment) OS=Homo sapiens OX=9606 GN=C1QB PE=1 SV=6
58	1	Human_Uniprot_2018	sp|P02748|CO9_HUMAN	132	64615	7	7	4	4	0.34	Complement component C9 OS=Homo sapiens OX=9606 GN=C9 PE=1 SV=2
59	1	Human_Uniprot_2018	sp|P06702|S10A9_HUMAN	130	13291	4	4	1	1	0.42	Protein S100-A9 OS=Homo sapiens OX=9606 GN=S100A9 PE=1 SV=1
60	1	Human_Uniprot_2018	sp|P07737|PROF1_HUMAN	129	15216	6	6	4	4	2.39	Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2
61	1	Human_Uniprot_2018	sp|A0A0C4DH38|HV551_HUMAN	128	12837	4	4	3	3	1.94	Immunoglobulin heavy variable 5-51 OS=Homo sapiens OX=9606 GN=IGHV5-51 PE=3 SV=1
62	1	Human_Uniprot_2018	sp|A0A075B6S5|KV127_HUMAN	127	12874	3	3	1	1	0.43	Immunoglobulin kappa variable 1-27 OS=Homo sapiens OX=9606 GN=IGKV1-27 PE=3 SV=1
63	1	Human_Uniprot_2018	tr|A0A2R8Y7C0|A0A2R8Y7C0_HUMAN	125	13945	8	8	3	3	1.7	Hemoglobin subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1
64	1	Human_Uniprot_2018	sp|P27169|PON1_HUMAN	124	39877	6	6	5	5	0.8	Serum paraoxonase/arylesterase 1 OS=Homo sapiens OX=9606 GN=PON1 PE=1 SV=3
65	1	Human_Uniprot_2018	sp|P02743|SAMP_HUMAN	123	25485	7	7	3	3	0.73	Serum amyloid P-component OS=Homo sapiens OX=9606 GN=APCS PE=1 SV=2
66	1	Human_Uniprot_2018	sp|A0A075B6K5|LV39_HUMAN	122	12438	1	1	1	1	0.45	Immunoglobulin lambda variable 3-9 OS=Homo sapiens OX=9606 GN=IGLV3-9 PE=3 SV=1
67	1	Human_Uniprot_2018	tr|B4E1Z4|B4E1Z4_HUMAN	122	143191	6	6	4	4	0.14	cDNA FLJ55673, highly similar to Complement factor B (EC 3.4.21.47) OS=Homo sapiens OX=9606 PE=1 SV=1
68	1	Human_Uniprot_2018	sp|P35579|MYH9_HUMAN	115	227646	10	10	8	8	0.18	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4
69	1	Human_Uniprot_2018	sp|P02750|A2GL_HUMAN	114	38382	6	6	5	5	0.84	Leucine-rich alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=LRG1 PE=1 SV=2
70	1	Human_Uniprot_2018	tr|Q5VY30|Q5VY30_HUMAN	113	23301	4	4	2	2	0.49	Retinol-binding protein OS=Homo sapiens OX=9606 GN=RBP4 PE=1 SV=2
71	1	Human_Uniprot_2018	tr|A0A087WWY3|A0A087WWY3_HUMAN	111	248149	7	7	6	6	0.12	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=1
72	1	Human_Uniprot_2018	sp|P43652|AFAM_HUMAN	111	70963	8	8	4	4	0.3	Afamin OS=Homo sapiens OX=9606 GN=AFM PE=1 SV=1
73	1	Human_Uniprot_2018	tr|A0A0J9YY99|A0A0J9YY99_HUMAN	104	13128	4	4	2	2	1.03	Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1
74	1	Human_Uniprot_2018	sp|P08185|CBG_HUMAN	99	45283	3	3	2	2	0.23	Corticosteroid-binding globulin OS=Homo sapiens OX=9606 GN=SERPINA6 PE=1 SV=1
75	1	Human_Uniprot_2018	sp|A0A0C4DH68|KV224_HUMAN	96	13185	4	4	2	2	1.01	Immunoglobulin kappa variable 2-24 OS=Homo sapiens OX=9606 GN=IGKV2-24 PE=3 SV=1
76	1	Human_Uniprot_2018	sp|P07996|TSP1_HUMAN	95	133291	4	4	4	4	0.15	Thrombospondin-1 OS=Homo sapiens OX=9606 GN=THBS1 PE=1 SV=2
77	1	Human_Uniprot_2018	sp|P01599|KV117_HUMAN	92	12941	3	3	2	2	1.04	Immunoglobulin kappa variable 1-17 OS=Homo sapiens OX=9606 GN=IGKV1-17 PE=1 SV=2
78	1	Human_Uniprot_2018	sp|Q96PD5-2|PGRP2_HUMAN	89	68699	6	6	4	4	0.32	Isoform 2 of N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens OX=9606 GN=PGLYRP2
79	1	Human_Uniprot_2018	tr|Q5JP53|Q5JP53_HUMAN	86	48135	4	4	3	3	0.34	Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=1
79	2	Human_Uniprot_2018	sp|Q9H4B7|TBB1_HUMAN	57	50865	2	2	2	2	0.2	Tubulin beta-1 chain OS=Homo sapiens OX=9606 GN=TUBB1 PE=1 SV=1
80	1	Human_Uniprot_2018	tr|S4R471|S4R471_HUMAN	78	21883	2	2	2	2	0.53	Protein AMBP (Fragment) OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1
81	1	Human_Uniprot_2018	sp|P06312|KV401_HUMAN	73	13486	3	3	1	1	0.41	Immunoglobulin kappa variable 4-1 OS=Homo sapiens OX=9606 GN=IGKV4-1 PE=1 SV=1
82	1	Human_Uniprot_2018	tr|H9KV75|H9KV75_HUMAN	70	95279	3	3	3	3	0.16	Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1
83	1	Human_Uniprot_2018	sp|P00747|PLMN_HUMAN	68	93247	3	3	2	2	0.11	Plasminogen OS=Homo sapiens OX=9606 GN=PLG PE=1 SV=2
84	1	Human_Uniprot_2018	sp|A0A075B6P5|KV228_HUMAN	67	13062	2	2	2	2	1.03	Immunoglobulin kappa variable 2-28 OS=Homo sapiens OX=9606 GN=IGKV2-28 PE=3 SV=1
85	1	Human_Uniprot_2018	tr|B4DPQ0|B4DPQ0_HUMAN	67	83376	6	6	5	5	0.33	cDNA FLJ54471, highly similar to Complement C1r subcomponent (EC 3.4.21.41) OS=Homo sapiens OX=9606 GN=C1R PE=1 SV=1
86	1	Human_Uniprot_2018	tr|E9PHK0|E9PHK0_HUMAN	60	18125	3	3	2	2	0.67	Tetranectin OS=Homo sapiens OX=9606 GN=CLEC3B PE=1 SV=1
87	1	Human_Uniprot_2018	tr|A0A0A0MS09|A0A0A0MS09_HUMAN	60	47966	1	1	1	1	0.1	Immunoglobulin heavy constant delta (Fragment) OS=Homo sapiens OX=9606 GN=IGHD PE=1 SV=1
88	1	Human_Uniprot_2018	sp|P04003|C4BPA_HUMAN	59	69042	5	5	3	3	0.23	C4b-binding protein alpha chain OS=Homo sapiens OX=9606 GN=C4BPA PE=1 SV=2
89	1	Human_Uniprot_2018	tr|A0A096LPE2|A0A096LPE2_HUMAN	59	23510	3	3	2	2	0.49	SAA2-SAA4 readthrough OS=Homo sapiens OX=9606 GN=SAA2-SAA4 PE=4 SV=1
90	1	Human_Uniprot_2018	sp|P43251-2|BTD_HUMAN	59	62383	2	2	2	2	0.16	Isoform 2 of Biotinidase OS=Homo sapiens OX=9606 GN=BTD
91	1	Human_Uniprot_2018	sp|A0A0J9YX35|HV64D_HUMAN	57	12985	2	2	1	1	0.43	Immunoglobulin heavy variable 3-64D OS=Homo sapiens OX=9606 GN=IGHV3-64D PE=3 SV=1
92	1	Human_Uniprot_2018	tr|K7ERI9|K7ERI9_HUMAN	57	8642	4	4	2	2	1.88	Apolipoprotein C-I (Fragment) OS=Homo sapiens OX=9606 GN=APOC1 PE=1 SV=1
93	1	Human_Uniprot_2018	sp|P01721|LV657_HUMAN	56	12729	2	2	1	1	0.44	Immunoglobulin lambda variable 6-57 OS=Homo sapiens OX=9606 GN=IGLV6-57 PE=1 SV=2
94	1	Human_Uniprot_2018	sp|P62328|TYB4_HUMAN	55	5050	2	2	1	1	1.45	Thymosin beta-4 OS=Homo sapiens OX=9606 GN=TMSB4X PE=1 SV=2
95	1	Human_Uniprot_2018	sp|P01700|LV147_HUMAN	55	12447	1	1	1	1	0.45	Immunoglobulin lambda variable 1-47 OS=Homo sapiens OX=9606 GN=IGLV1-47 PE=1 SV=2
96	1	Human_Uniprot_2018	sp|P10643|CO7_HUMAN	54	96650	2	2	2	2	0.1	Complement component C7 OS=Homo sapiens OX=9606 GN=C7 PE=1 SV=2

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
97	1	Human_Uniprot_2018	sp|P05546|HEP2_HUMAN	52	57205	4	4	4	4	0.39	Heparin cofactor 2 OS=Homo sapiens OX=9606 GN=SERPIND1 PE=1 SV=3
98	1	Human_Uniprot_2018	tr|A0A2R8Y3M9|A0A2R8Y3M9_HUMAN	50	74186	2	2	1	1	0.07	Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1
99	1	Human_Uniprot_2018	tr|A0A087X232|A0A087X232_HUMAN	49	77396	2	2	2	2	0.13	Complement C1s subcomponent OS=Homo sapiens OX=9606 GN=C1S PE=1 SV=1
100	1	Human_Uniprot_2018	tr|F5H1C6|F5H1C6_HUMAN	43	33292	1	1	1	1	0.15	Fermitin family homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=FERMT3 PE=1 SV=1
101	1	Human_Uniprot_2018	sp|P29622|KAIN_HUMAN	42	48682	1	1	1	1	0.1	Kallistatin OS=Homo sapiens OX=9606 GN=SERPINA4 PE=1 SV=3
102	1	Human_Uniprot_2018	sp|A0A0C4DH31|HV118_HUMAN	42	12926	3	3	2	2	1.05	Immunoglobulin heavy variable 1-18 OS=Homo sapiens OX=9606 GN=IGHV1-18 PE=3 SV=1
103	1	Human_Uniprot_2018	tr|Q5H928|Q5H928_HUMAN	41	17498	3	3	1	1	0.3	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=1
104	1	Human_Uniprot_2018	tr|Q5SQ08|Q5SQ08_HUMAN	39	17660	1	1	1	1	0.3	Complement component C8 gamma chain (Fragment) OS=Homo sapiens OX=9606 GN=C8G PE=1 SV=1
105	1	Human_Uniprot_2018	sp|P51884|LUM_HUMAN	36	38747	2	2	2	2	0.27	Lumican OS=Homo sapiens OX=9606 GN=LUM PE=1 SV=2
106	1	Human_Uniprot_2018	tr|A0A087X1J7|A0A087X1J7_HUMAN	35	25614	2	2	2	2	0.44	Glutathione peroxidase OS=Homo sapiens OX=9606 GN=GPX3 PE=1 SV=1
107	1	Human_Uniprot_2018	sp|P00488|F13A_HUMAN	35	83728	1	1	1	1	0.06	Coagulation factor XIII A chain OS=Homo sapiens OX=9606 GN=F13A1 PE=1 SV=4
108	1	Human_Uniprot_2018	sp|P08514-2|ITA2B_HUMAN	35	110645	2	2	2	2	0.09	Isoform 2 of Integrin alpha-IIb OS=Homo sapiens OX=9606 GN=ITGA2B
109	1	Human_Uniprot_2018	sp|A0A0A0MS15|HV349_HUMAN	34	13219	2	2	1	1	0.42	Immunoglobulin heavy variable 3-49 OS=Homo sapiens OX=9606 GN=IGHV3-49 PE=3 SV=1
110	1	Human_Uniprot_2018	sp|A0A0A0MRZ8|KVD11_HUMAN	33	12731	1	1	1	1	0.44	Immunoglobulin kappa variable 3D-11 OS=Homo sapiens OX=9606 GN=IGKV3D-11 PE=3 SV=6
111	1	Human_Uniprot_2018	sp|P01031|CO5_HUMAN	33	189897	3	3	2	2	0.05	Complement C5 OS=Homo sapiens OX=9606 GN=C5 PE=1 SV=4
112	1	Human_Uniprot_2018	tr|K7EQQ3|K7EQQ3_HUMAN	33	39618	2	2	2	2	0.27	Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=1
113	1	Human_Uniprot_2018	tr|A0A075B6Z2|A0A075B6Z2_HUMAN	32	2220	1	1	1	1	5.73	T cell receptor alpha joining 56 (Fragment) OS=Homo sapiens OX=9606 GN=TRAJ56 PE=4 SV=1
114	1	Human_Uniprot_2018	tr|G3V1V0|G3V1V0_HUMAN	30	18311	1	1	1	1	0.29	Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1
115	1	Human_Uniprot_2018	sp|P36955|PEDF_HUMAN	30	46454	2	2	2	2	0.22	Pigment epithelium-derived factor OS=Homo sapiens OX=9606 GN=SERPINF1 PE=1 SV=4
116	1	Human_Uniprot_2018	tr|E9PI65|E9PI65_HUMAN	29	17962	1	1	1	1	0.3	Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1
117	1	Human_Uniprot_2018	tr|F5GZG1|F5GZG1_HUMAN	29	13937	1	1	1	1	0.39	Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=8
118	1	Human_Uniprot_2018	sp|Q7Z7A1-5|CNTRL_HUMAN	28	269216	1	1	1	1	0.02	Isoform 5 of Centriolin OS=Homo sapiens OX=9606 GN=CNTRL
119	1	Human_Uniprot_2018	sp|P00748|FA12_HUMAN	27	70029	1	1	1	1	0.07	Coagulation factor XII OS=Homo sapiens OX=9606 GN=F12 PE=1 SV=3
120	1	Human_Uniprot_2018	sp|P01742|HV169_HUMAN	26	12765	1	1	1	1	0.44	Immunoglobulin heavy variable 1-69 OS=Homo sapiens OX=9606 GN=IGHV1-69 PE=1 SV=2
121	1	Human_Uniprot_2018	sp|Q7Z2Y8|GVIN1_HUMAN	26	281950	1	1	1	1	0.02	**Interferon-induced very large GTPase 1 OS=Homo sapiens OX=9606 GN=GVINP1 PE=2 SV=2**
122	1	Human_Uniprot_2018	tr|G5E9F8|G5E9F8_HUMAN	25	61914	1	1	1	1	0.08	Protein S (Alpha), isoform CRA_b OS=Homo sapiens OX=9606 GN=PROS1 PE=1 SV=1
123	1	Human_Uniprot_2018	sp|Q4U2R6|RM51_HUMAN	25	15199	1	1	1	1	0.36	39S ribosomal protein L51, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL51 PE=1 SV=1
124	1	Human_Uniprot_2018	tr|A0A0C4DH36|A0A0C4DH36_HUMAN	24	12921	1	1	1	1	0.43	Immunoglobulin heavy variable 3-38 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV3-38 PE=1 SV=1
125	1	Human_Uniprot_2018	sp|A0A0B4J1Y9|HV372_HUMAN	23	13366	1	1	1	1	0.42	Immunoglobulin heavy variable 3-72 OS=Homo sapiens OX=9606 GN=IGHV3-72 PE=3 SV=1
126	1	Human_Uniprot_2018	tr|A0A096LPE1|A0A096LPE1_HUMAN	23	6083	2	2	1	1	1.1	Vinculin OS=Homo sapiens OX=9606 GN=VCL PE=1 SV=1
127	1	Human_Uniprot_2018	sp|Q86SG5|S1A7A_HUMAN	23	11412	1	1	1	1	0.5	Protein S100-A7A OS=Homo sapiens OX=9606 GN=S100A7A PE=1 SV=3
128	1	Human_Uniprot_2018	sp|Q9HCK5|AGO4_HUMAN	22	98175	1	1	1	1	0.05	Protein argonaute-4 OS=Homo sapiens OX=9606 GN=AGO4 PE=1 SV=2
129	1	Human_Uniprot_2018	tr|E5RK49|E5RK49_HUMAN	22	24286	1	1	1	1	0.21	F-BAR and double SH3 domains protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=FCHSD1 PE=1 SV=1
130	1	Human_Uniprot_2018	sp|P15814|IGLL1_HUMAN	22	23177	1	1	1	1	0.22	Immunoglobulin lambda-like polypeptide 1 OS=Homo sapiens OX=9606 GN=IGLL1 PE=1 SV=1
131	1	Human_Uniprot_2018	tr|X6RJP6|X6RJP6_HUMAN	21	21244	1	1	1	1	0.25	Transgelin-2 (Fragment) OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=1
132	1	Human_Uniprot_2018	sp|Q7Z5J8-2|ANKAR_HUMAN	20	124301	1	1	1	1	0.04	Isoform 2 of Ankyrin and armadillo repeat-containing protein OS=Homo sapiens OX=9606 GN=ANKAR
133	1	Human_Uniprot_2018	sp|P02747|C1QC_HUMAN	19	25985	1	1	1	1	0.2	Actinin OS=Homo sapiens OX=9606 GN=C1QC PE=1 SV=3
134	1	Human_Uniprot_2018	sp|O60292|SI1L3_HUMAN	19	195801	1	1	1	1	0.02	Signal-induced proliferation-associated 1-like protein 3 OS=Homo sapiens OX=9606 GN=SIPA1L3 PE=1 SV=3
135	1	Human_Uniprot_2018	sp|Q96JK9|MAML3_HUMAN	19	122673	1	1	1	1	0.04	Mastermind-like protein 3 OS=Homo sapiens OX=9606 GN=MAML3 PE=1 SV=4
136	1	Human_Uniprot_2018	tr|A0A0J9YYC8|A0A0J9YYC8_HUMAN	19	26867	1	1	1	1	0.19	Trypsin-2 OS=Homo sapiens OX=9606 GN=PRSS2 PE=1 SV=1
137	1	Human_Uniprot_2018	sp|Q5W0B1|RN219_HUMAN	19	82377	1	1	1	1	0.06	RING finger protein 219 OS=Homo sapiens OX=9606 GN=RNF219 PE=1 SV=1
138	1	Human_Uniprot_2018	tr|C9JF17|C9JF17_HUMAN	18	24541	1	1	1	1	0.21	Apolipoprotein D (Fragment) OS=Homo sapiens OX=9606 GN=APOD PE=1 SV=1
139	1	Human_Uniprot_2018	tr|A0A2R8Y6G6|A0A2R8Y6G6_HUMAN	18	47696	1	1	1	1	0.1	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1
140	1	Human_Uniprot_2018	sp|Q9C0B9|ZCHC2_HUMAN	18	126998	1	1	1	1	0.04	Zinc finger CCHC domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ZCCHC2 PE=1 SV=6
141	1	Human_Uniprot_2018	sp|P08567|PLEK_HUMAN	18	40499	1	1	1	1	0.12	Pleckstrin OS=Homo sapiens OX=9606 GN=PLEK PE=1 SV=3
142	1	Human_Uniprot_2018	sp|P0DPH7-2|TBA3C_HUMAN	18	46767	1	1	1	1	0.11	Isoform 2 of Tubulin alpha-3C chain OS=Homo sapiens OX=9606 GN=TUBA3C

	WITH PAS - DAY 5 2(a)										
Family	**Member**	**Database**	**Accession**	**Score**	**Mass**	**Num. of matches**	**Num. of significant matches**	**Num. of sequences**	**Num. of significant sequences**	**emPAI**	**Description**
1	1	Human_Uniprot_2018	sp|P02768|ALBU_HUMAN	5567	71317	267	267	23	23	3.88	Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2
2	1	Human_Uniprot_2018	sp|P01024|CO3_HUMAN	3278	188569	119	119	39	39	1.65	Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2
3	1	Human_Uniprot_2018	sp|P02647|APOA1_HUMAN	1786	30759	70	70	20	20	20.01	Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1
4	1	Human_Uniprot_2018	sp|P01009|A1AT_HUMAN	1736	46878	62	62	15	15	3.5	Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3
5	1	Human_Uniprot_2018	sp|P01023|A2MG_HUMAN	1660	164613	80	80	29	29	1.29	Alpha-2-macroglobulin OS=Homo sapiens OX=9606 GN=A2M PE=1 SV=3
6	1	Human_Uniprot_2018	tr|A0A0A0MS08|A0A0A0MS08_HUMAN	1478	44511	70	70	8	8	1.32	Immunoglobulin heavy constant gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1
6	2	Human_Uniprot_2018	sp|P01859|IGHG2_HUMAN	670	36505	42	42	4	4	0.9	Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=2
6	3	Human_Uniprot_2018	sp|P01861|IGHG4_HUMAN	669	36431	21	21	5	5	0.9	Immunoglobulin heavy constant gamma 4 OS=Homo sapiens OX=9606 GN=IGHG4 PE=1 SV=1
6	4	Human_Uniprot_2018	sp|P01860|IGHG3_HUMAN	615	42287	36	36	5	5	0.74	Immunoglobulin heavy constant gamma 3 OS=Homo sapiens OX=9606 GN=IGHG3 PE=1 SV=2
7	1	Human_Uniprot_2018	sp|P02787|TRFE_HUMAN	1379	79294	63	63	17	17	1.74	Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=3
8	1	Human_Uniprot_2018	sp|P04114|APOB_HUMAN	1263	516651	76	76	53	53	0.62	Apolipoprotein B-100 OS=Homo sapiens OX=9606 GN=APOB PE=1 SV=2
9	1	Human_Uniprot_2018	sp|P01834|IGKC_HUMAN	1243	11929	49	49	5	5	5.98	Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2
10	1	Human_Uniprot_2018	sp|P0C0L5|CO4B_HUMAN	1192	194170	40	40	21	21	0.67	Complement C4-B OS=Homo sapiens OX=9606 GN=C4B PE=1 SV=2
10	2	Human_Uniprot_2018	tr|A0A0G2JPR0|A0A0G2JPR0_HUMAN	1103	194351	38	38	20	20	0.62	Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=1
11	1	Human_Uniprot_2018	sp|P02675|FIBB_HUMAN	1191	56577	55	55	17	17	3.1	Fibrinogen beta chain OS=Homo sapiens OX=9606 GN=FGB PE=1 SV=2
12	1	Human_Uniprot_2018	sp|P02671-2|FIBA_HUMAN	1129	70227	48	48	12	12	1.23	Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA
13	1	Human_Uniprot_2018	sp|P02766|TTHY_HUMAN	958	15991	38	38	10	10	17.26	Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1
14	1	Human_Uniprot_2018	sp|P02751-10|FINC_HUMAN	733	243068	30	30	17	17	0.39	Isoform 10 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1
15	1	Human_Uniprot_2018	tr|A0A1B0GUU9|A0A1B0GUU9_HUMAN	625	52518	28	28	5	5	0.56	Immunoglobulin heavy constant mu (Fragment) OS=Homo sapiens OX=9606 GN=IGHM PE=1 SV=1
16	1	Human_Uniprot_2018	tr|C9JC84|C9JC84_HUMAN	620	52932	26	26	8	8	1.03	Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=1
17	1	Human_Uniprot_2018	sp|P01011|AACT_HUMAN	591	47792	21	21	9	9	1.42	Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=2
18	1	Human_Uniprot_2018	sp|A0M8Q6|IGLC7_HUMAN	511	11418	19	19	2	2	1.24	Immunoglobulin lambda constant 7 OS=Homo sapiens OX=9606 GN=IGLC7 PE=1 SV=3
18	2	Human_Uniprot_2018	sp|B9A064|IGLL5_HUMAN	363	23391	14	14	3	3	0.82	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens OX=9606 GN=IGLL5 PE=2 SV=2
19	1	Human_Uniprot_2018	sp|P00450|CERU_HUMAN	499	122983	28	28	14	14	0.71	Ceruloplasmin OS=Homo sapiens OX=9606 GN=CP PE=1 SV=1
20	1	Human_Uniprot_2018	tr|A0A286YEY1|A0A286YEY1_HUMAN	496	43620	12	12	2	2	0.24	Immunoglobulin heavy constant alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=1
20	2	Human_Uniprot_2018	tr|A0A0G2JMB2|A0A0G2JMB2_HUMAN	418	37283	10	10	2	2	0.29	Immunoglobulin heavy constant alpha 2 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA2 PE=1 SV=1
21	1	Human_Uniprot_2018	sp|P60709|ACTB_HUMAN	430	42052	18	18	9	9	1.73	Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1
21	2	Human_Uniprot_2018	sp|P62736|ACTA_HUMAN	193	42381	12	12	6	6	0.94	Actin, aortic smooth muscle OS=Homo sapiens OX=9606 GN=ACTA2 PE=1 SV=1
22	1	Human_Uniprot_2018	sp|P04264|K2C1_HUMAN	369	66170	14	14	9	9	0.9	Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6
22	2	Human_Uniprot_2018	sp|P35908|K22E_HUMAN	114	65678	3	3	2	2	0.15	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2
22	3	Human_Uniprot_2018	sp|P04259|K2C6B_HUMAN	101	60315	3	3	2	2	0.17	Keratin, type II cytoskeletal 6B OS=Homo sapiens OX=9606 GN=KRT6B PE=1 SV=5
23	1	Human_Uniprot_2018	sp|P68871|HBB_HUMAN	345	16102	10	10	6	6	4.65	Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2
24	1	Human_Uniprot_2018	tr|J3QLC9|J3QLC9_HUMAN	333	41381	14	14	6	6	0.97	Haptoglobin (Fragment) OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1
25	1	Human_Uniprot_2018	sp|P01008|ANT3_HUMAN	327	53025	12	12	6	6	0.7	Antithrombin-III OS=Homo sapiens OX=9606 GN=SERPINC1 PE=1 SV=1
26	1	Human_Uniprot_2018	tr|D6RF35|D6RF35_HUMAN	327	54583	20	20	6	6	0.68	Vitamin D-binding protein OS=Homo sapiens OX=9606 GN=GC PE=1 SV=1
27	1	Human_Uniprot_2018	tr|B7ZKJ8|B7ZKJ8_HUMAN	322	104044	19	19	14	14	0.89	ITIH4 protein OS=Homo sapiens OX=9606 GN=ITIH4 PE=1 SV=1
28	1	Human_Uniprot_2018	sp|P19827|ITIH1_HUMAN	310	101782	12	12	8	8	0.45	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens OX=9606 GN=ITIH1 PE=1 SV=3
29	1	Human_Uniprot_2018	sp|P02763|A1AG1_HUMAN	304	23725	18	18	5	5	1.67	Alpha-1-acid glycoprotein 1 OS=Homo sapiens OX=9606 GN=ORM1 PE=1 SV=1
29	2	Human_Uniprot_2018	sp|P19652|A1AG2_HUMAN	78	23873	5	5	2	2	0.48	Alpha-1-acid glycoprotein 2 OS=Homo sapiens OX=9606 GN=ORM2 PE=1 SV=2
30	1	Human_Uniprot_2018	sp|P01619|KV320_HUMAN	299	12663	6	6	2	2	1.08	Immunoglobulin kappa variable 3-20 OS=Homo sapiens OX=9606 GN=IGKV3-20 PE=1 SV=2

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
31	1	Human_Uniprot_2018	tr|A0A2Q2TTZ9|A0A2Q2TTZ9_HUMAN	293	11949	5	5	2	2	1.16	Immunoglobulin kappa variable 1-33 OS=Homo sapiens OX=9606 GN=IGKV1D-33 PE=1 SV=1
32	1	Human_Uniprot_2018	sp|P06727|APOA4_HUMAN	284	45371	16	16	8	8	1.29	Apolipoprotein A-IV OS=Homo sapiens OX=9606 GN=APOA4 PE=1 SV=3
33	1	Human_Uniprot_2018	sp|P04004|VTNC_HUMAN	268	55069	7	7	3	3	0.29	Vitronectin OS=Homo sapiens OX=9606 GN=VTN PE=1 SV=1
34	1	Human_Uniprot_2018	sp|P02790|HEMO_HUMAN	254	52385	15	15	7	7	0.87	Hemopexin OS=Homo sapiens OX=9606 GN=HPX PE=1 SV=2
35	1	Human_Uniprot_2018	sp|P02649|APOE_HUMAN	245	36246	11	11	6	6	1.17	Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1
36	1	Human_Uniprot_2018	tr|B0YIW2|B0YIW2_HUMAN	241	12864	6	6	3	3	1.94	Apolipoprotein C-III variant 1 OS=Homo sapiens OX=9606 GN=APOC3 PE=1 SV=1
37	1	Human_Uniprot_2018	sp|A0A075B6K5|LV39_HUMAN	228	12438	2	2	1	1	0.45	Immunoglobulin lambda variable 3-9 OS=Homo sapiens OX=9606 GN=IGLV3-9 PE=3 SV=1
38	1	Human_Uniprot_2018	sp|P04196|HRG_HUMAN	224	60510	7	7	4	4	0.36	Histidine-rich glycoprotein OS=Homo sapiens OX=9606 GN=HRG PE=1 SV=1
39	1	Human_Uniprot_2018	sp|P01042-2|KNG1_HUMAN	224	48936	6	6	3	3	0.33	Isoform LMW of Kininogen-1 OS=Homo sapiens OX=9606 GN=KNG1
40	1	Human_Uniprot_2018	sp|P10909-2|CLUS_HUMAN	218	58537	12	12	5	5	0.49	Isoform 2 of Clusterin OS=Homo sapiens OX=9606 GN=CLU
41	1	Human_Uniprot_2018	tr|A0A0A0MS51|A0A0A0MS51_HUMAN	217	82759	13	13	7	7	0.49	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
42	1	Human_Uniprot_2018	tr|E9PIT3|E9PIT3_HUMAN	204	66792	7	7	4	4	0.33	Prothrombin OS=Homo sapiens OX=9606 GN=F2 PE=1 SV=1
43	1	Human_Uniprot_2018	tr|A0A0B4J2B5|A0A0B4J2B5_HUMAN	201	10764	7	7	2	2	1.35	Immunoglobulin heavy variable 3/OR16-9 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV3OR16-9 PE=1 SV=1
44	1	Human_Uniprot_2018	tr|C9JEV0|C9JEV0_HUMAN	200	26508	8	8	4	4	1.02	Zinc-alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=AZGP1 PE=1 SV=1
45	1	Human_Uniprot_2018	tr|E9PGN7|E9PGN7_HUMAN	196	59683	7	7	5	5	0.48	Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1 PE=1 SV=1
46	1	Human_Uniprot_2018	sp|P08603|CFAH_HUMAN	183	143680	9	9	5	5	0.18	Complement factor H OS=Homo sapiens OX=9606 GN=CFH PE=1 SV=4
47	1	Human_Uniprot_2018	tr|Q5T985|Q5T985_HUMAN	181	105606	11	11	7	7	0.37	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens OX=9606 GN=ITIH2 PE=1 SV=1
48	1	Human_Uniprot_2018	tr|C9JV77|C9JV77_HUMAN	153	40185	4	4	1	1	0.12	Alpha-2-HS-glycoprotein OS=Homo sapiens OX=9606 GN=AHSG PE=1 SV=1
49	1	Human_Uniprot_2018	sp|P01019|ANGT_HUMAN	145	53406	7	7	5	5	0.55	Angiotensinogen OS=Homo sapiens OX=9606 GN=AGT PE=1 SV=1
50	1	Human_Uniprot_2018	tr|V9GYE3|V9GYE3_HUMAN	137	5873	3	3	2	2	3.63	Apolipoprotein A-II OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1
51	1	Human_Uniprot_2018	sp|P04217|A1BG_HUMAN	135	54790	10	10	6	6	0.67	Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=4
52	1	Human_Uniprot_2018	tr|A0A0A0MSV6|A0A0A0MSV6_HUMAN	120	24243	5	5	3	3	0.78	Complement C1q subcomponent subunit B (Fragment) OS=Homo sapiens OX=9606 GN=C1QB PE=1 SV=6
53	1	Human_Uniprot_2018	sp|P07996|TSP1_HUMAN	107	133291	4	4	4	4	0.15	Thrombospondin-1 OS=Homo sapiens OX=9606 GN=THBS1 PE=1 SV=2
54	1	Human_Uniprot_2018	sp|P02743|SAMP_HUMAN	106	25485	6	6	3	3	0.73	Serum amyloid P-component OS=Homo sapiens OX=9606 GN=APCS PE=1 SV=2
55	1	Human_Uniprot_2018	tr|S4R471|S4R471_HUMAN	104	21883	4	4	3	3	0.9	Protein AMBP (Fragment) OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1
56	1	Human_Uniprot_2018	sp|P27169|PON1_HUMAN	100	39877	5	5	4	4	0.6	Serum paraoxonase/arylesterase 1 OS=Homo sapiens OX=9606 GN=PON1 PE=1 SV=3
57	1	Human_Uniprot_2018	sp|P62328|TYB4_HUMAN	99	5050	2	2	1	1	1.45	Thymosin beta-4 OS=Homo sapiens OX=9606 GN=TMSB4X PE=1 SV=2
58	1	Human_Uniprot_2018	tr|B4E1Z4|B4E1Z4_HUMAN	99	143191	3	3	2	2	0.07	cDNA FLJ55673, highly similar to Complement factor B (EC 3.4.21.47) OS=Homo sapiens OX=9606 PE=1 SV=1
59	1	Human_Uniprot_2018	tr|A0A0J9YY99|A0A0J9YY99_HUMAN	96	13128	4	4	2	2	1.03	Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1
60	1	Human_Uniprot_2018	tr|A0A024R0T9|A0A024R0T9_HUMAN	94	11277	3	3	2	2	1.26	Apolipoprotein C-II isoform 1 OS=Homo sapiens OX=9606 GN=APOC4-APOC2 PE=1 SV=1
61	1	Human_Uniprot_2018	sp|P04003|C4BPA_HUMAN	93	69042	3	3	2	2	0.15	C4b-binding protein alpha chain OS=Homo sapiens OX=9606 GN=C4BPA PE=1 SV=2
62	1	Human_Uniprot_2018	sp|P02748|CO9_HUMAN	93	64615	3	3	2	2	0.16	Complement component C9 OS=Homo sapiens OX=9606 GN=C9 PE=1 SV=2
63	1	Human_Uniprot_2018	sp|P07737|PROF1_HUMAN	84	15216	3	3	3	3	1.5	Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2
64	1	Human_Uniprot_2018	sp|P01599|KV117_HUMAN	83	12941	2	2	2	2	1.04	Immunoglobulin kappa variable 1-17 OS=Homo sapiens OX=9606 GN=IGKV1-17 PE=1 SV=2
65	1	Human_Uniprot_2018	tr|A0A2R8Y7C0|A0A2R8Y7C0_HUMAN	81	13945	7	7	4	4	2.76	Hemoglobin subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1
66	1	Human_Uniprot_2018	tr|Q5VY30|Q5VY30_HUMAN	80	23301	4	4	2	2	0.49	Retinol-binding protein OS=Homo sapiens OX=9606 GN=RBP4 PE=1 SV=2
67	1	Human_Uniprot_2018	tr|A0A0G2JPA8|A0A0G2JPA8_HUMAN	79	48135	5	5	3	3	0.34	Alpha-2-antiplasmin OS=Homo sapiens OX=9606 GN=SERPINF2 PE=1 SV=1
68	1	Human_Uniprot_2018	sp|A0A075B6S5|KV127_HUMAN	79	12874	1	1	1	1	0.43	Immunoglobulin kappa variable 1-27 OS=Homo sapiens OX=9606 GN=IGKV1-27 PE=3 SV=1
69	1	Human_Uniprot_2018	sp|P02775|CXCL7_HUMAN	77	14171	4	4	2	2	0.92	Platelet basic protein OS=Homo sapiens OX=9606 GN=PPBP PE=1 SV=3

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
70	1	Human_Uniprot_2018	sp|P13645|K1C10_HUMAN	75	59020	2	2	2	2	0.17	Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6
71	1	Human_Uniprot_2018	tr|C9JF17|C9JF17_HUMAN	73	24541	4	4	2	2	0.46	Apolipoprotein D (Fragment) OS=Homo sapiens OX=9606 GN=APOD PE=1 SV=1
72	1	Human_Uniprot_2018	tr|K7EQQ3|K7EQQ3_HUMAN	71	39618	3	3	3	3	0.43	Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=1
73	1	Human_Uniprot_2018	tr|A0A087X232|A0A087X232_HUMAN	66	77396	1	1	1	1	0.06	Complement C1s subcomponent OS=Homo sapiens OX=9606 GN=C1S PE=1 SV=1
74	1	Human_Uniprot_2018	sp|P80108|PHLD_HUMAN	64	92905	1	1	1	1	0.05	Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens OX=9606 GN=GPLD1 PE=1 SV=3
75	1	Human_Uniprot_2018	sp|A0A0J9YX35|HV64D_HUMAN	64	12985	2	2	1	1	0.43	Immunoglobulin heavy variable 3-64D OS=Homo sapiens OX=9606 GN=IGHV3-64D PE=3 SV=1
76	1	Human_Uniprot_2018	sp|Q9Y490|TLN1_HUMAN	63	271766	4	4	4	4	0.07	Talin-1 OS=Homo sapiens OX=9606 GN=TLN1 PE=1 SV=3
77	1	Human_Uniprot_2018	tr|K7ERI9|K7ERI9_HUMAN	61	8642	2	2	2	2	1.88	Apolipoprotein C-I (Fragment) OS=Homo sapiens OX=9606 GN=APOC1 PE=1 SV=1
78	1	Human_Uniprot_2018	sp|A0A0C4DH72|KV106_HUMAN	59	12860	3	3	1	1	0.43	Immunoglobulin kappa variable 1-6 OS=Homo sapiens OX=9606 GN=IGKV1-6 PE=3 SV=1
79	1	Human_Uniprot_2018	tr|A0A087WWY3|A0A087WWY3_HUMAN	59	248149	6	6	5	5	0.1	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=1
80	1	Human_Uniprot_2018	tr|I3L2R7|I3L2R7_HUMAN	56	14121	2	2	2	2	0.93	Pigment epithelium-derived factor (Fragment) OS=Homo sapiens OX=9606 GN=SERPINF1 PE=1 SV=1
81	1	Human_Uniprot_2018	tr|A0A2R8Y3M9|A0A2R8Y3M9_HUMAN	54	74186	3	3	2	2	0.14	Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1
82	1	Human_Uniprot_2018	sp|P02750|A2GL_HUMAN	53	38382	2	2	1	1	0.13	Leucine-rich alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=LRG1 PE=1 SV=2
83	1	Human_Uniprot_2018	sp|P18206-2|VINC_HUMAN	52	117220	1	1	1	1	0.04	Isoform 1 of Vinculin OS=Homo sapiens OX=9606 GN=VCL
84	1	Human_Uniprot_2018	sp|A0A0C4DH68|KV224_HUMAN	52	13185	1	1	1	1	0.42	Immunoglobulin kappa variable 2-24 OS=Homo sapiens OX=9606 GN=IGKV2-24 PE=3 SV=1
85	1	Human_Uniprot_2018	sp|P43652|AFAM_HUMAN	49	70963	4	4	3	3	0.22	Afamin OS=Homo sapiens OX=9606 GN=AFM PE=1 SV=1
86	1	Human_Uniprot_2018	sp|A0A0B4J1V0|HV315_HUMAN	48	13089	1	1	1	1	0.42	Immunoglobulin heavy variable 3-15 OS=Homo sapiens OX=9606 GN=IGHV3-15 PE=3 SV=1
87	1	Human_Uniprot_2018	sp|A0A087WSY6|KVD15_HUMAN	46	12640	1	1	1	1	0.44	Immunoglobulin kappa variable 3D-15 OS=Homo sapiens OX=9606 GN=IGKV3D-15 PE=3 SV=6
88	1	Human_Uniprot_2018	tr|H0YJ11|H0YJ11_HUMAN	46	24359	4	4	2	2	0.47	Alpha-actinin-1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1
89	1	Human_Uniprot_2018	sp|P00747|PLMN_HUMAN	45	93247	2	2	1	1	0.05	Plasminogen OS=Homo sapiens OX=9606 GN=PLG PE=1 SV=2
90	1	Human_Uniprot_2018	sp|P06312|KV401_HUMAN	43	13486	2	2	1	1	0.41	Immunoglobulin kappa variable 4-1 OS=Homo sapiens OX=9606 GN=IGKV4-1 PE=1 SV=1
91	1	Human_Uniprot_2018	sp|P02747|C1QC_HUMAN	43	25985	1	1	1	1	0.2	Complement C1q subcomponent subunit C OS=Homo sapiens OX=9606 GN=C1QC PE=1 SV=3
92	1	Human_Uniprot_2018	sp|P05546|HEP2_HUMAN	42	57205	4	4	3	3	0.28	Heparin cofactor 2 OS=Homo sapiens OX=9606 GN=SERPIND1 PE=1 SV=3
93	1	Human_Uniprot_2018	tr|A0A075B7D0|A0A075B7D0_HUMAN	41	13117	1	1	1	1	0.42	Immunoglobulin heavy variable 1/OR15-1 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV1OR15-1 PE=1 SV=1
94	1	Human_Uniprot_2018	sp|A0A0A0MRZ8|KVD11_HUMAN	40	12731	1	1	1	1	0.44	Immunoglobulin kappa variable 3D-11 OS=Homo sapiens OX=9606 GN=IGKV3D-11 PE=3 SV=6
95	1	Human_Uniprot_2018	tr|B4DPQ0|B4DPQ0_HUMAN	40	83376	3	3	3	3	0.18	cDNA FLJ54471, highly similar to Complement C1r subcomponent (EC 3.4.21.41) OS=Homo sapiens OX=9606 GN=C1R PE=1 SV=1
96	1	Human_Uniprot_2018	tr|Q5H928|Q5H928_HUMAN	40	17498	2	2	1	1	0.3	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=1
97	1	Human_Uniprot_2018	sp|Q96PD5-2|PGRP2_HUMAN	38	68699	3	3	2	2	0.15	Isoform 2 of N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens OX=9606 GN=PGLYRP2
98	1	Human_Uniprot_2018	sp|P51884|LUM_HUMAN	38	38747	1	1	1	1	0.13	Lumican OS=Homo sapiens OX=9606 GN=LUM PE=1 SV=2
99	1	Human_Uniprot_2018	sp|P01031|CO5_HUMAN	38	189897	2	2	2	2	0.05	Complement C5 OS=Homo sapiens OX=9606 GN=C5 PE=1 SV=4
100	1	Human_Uniprot_2018	sp|A0A0C4DH38|HV551_HUMAN	37	12837	1	1	1	1	0.43	Immunoglobulin heavy variable 5-51 OS=Homo sapiens OX=9606 GN=IGHV5-51 PE=3 SV=1
101	1	Human_Uniprot_2018	sp|P08185|CBG_HUMAN	36	45283	1	1	1	1	0.11	Corticosteroid-binding globulin OS=Homo sapiens OX=9606 GN=SERPINA6 PE=1 SV=1
102	1	Human_Uniprot_2018	tr|A0A075B736|A0A075B736_HUMAN	35	46180	2	2	1	1	0.11	Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB8 PE=1 SV=1
103	1	Human_Uniprot_2018	sp|P10643|CO7_HUMAN	35	96650	1	1	1	1	0.05	Complement component C7 OS=Homo sapiens OX=9606 GN=C7 PE=1 SV=2
104	1	Human_Uniprot_2018	sp|P23083|HV102_HUMAN	33	13190	1	1	1	1	0.42	Immunoglobulin heavy variable 1-2 OS=Homo sapiens OX=9606 GN=IGHV1-2 PE=1 SV=2

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
105	1	Human_Uniprot_2018	tr|H0YAC1|H0YAC1_HUMAN	33	79001	2	2	2	2	0.13	Plasma kallikrein (Fragment) OS=Homo sapiens OX=9606 GN=KLKB1 PE=1 SV=1
106	1	Human_Uniprot_2018	sp|Q7Z7A1-5|CNTRL_HUMAN	31	269216	1	1	1	1	0.02	Isoform 5 of Centriolin OS=Homo sapiens OX=9606 GN=CNTRL
107	1	Human_Uniprot_2018	tr|E9PHK0|E9PHK0_HUMAN	31	18125	1	1	1	1	0.29	Tetranectin OS=Homo sapiens OX=9606 GN=CLEC3B PE=1 SV=1
108	1	Human_Uniprot_2018	sp|P00742|FA10_HUMAN	31	56065	1	1	1	1	0.09	Coagulation factor X OS=Homo sapiens OX=9606 GN=F10 PE=1 SV=2
109	1	Human_Uniprot_2018	tr|B1AN99|B1AN99_HUMAN	29	19561	1	1	1	1	0.27	Trypsin-3 (Fragment) OS=Homo sapiens OX=9606 GN=PRSS3 PE=1 SV=8
110	1	Human_Uniprot_2018	tr|F5GY80|F5GY80_HUMAN	29	61485	1	1	1	1	0.08	Complement component C8 beta chain OS=Homo sapiens OX=9606 GN=C8B PE=1 SV=1
111	1	Human_Uniprot_2018	tr|A0A087X1J7|A0A087X1J7_HUMAN	28	25614	1	1	1	1	0.2	Glutathione peroxidase OS=Homo sapiens OX=9606 GN=GPX3 PE=1 SV=1
112	1	Human_Uniprot_2018	sp|A0A075B6P5|KV228_HUMAN	28	13062	1	1	1	1	0.42	Immunoglobulin kappa variable 2-28 OS=Homo sapiens OX=9606 GN=IGKV2-28 PE=3 SV=1
113	1	Human_Uniprot_2018	tr|A0A0A0MS09|A0A0A0MS09_HUMAN	27	47966	1	1	1	1	0.1	Immunoglobulin heavy constant delta (Fragment) OS=Homo sapiens OX=9606 GN=IGHD PE=1 SV=1
114	1	Human_Uniprot_2018	sp|P35579-2|MYH9_HUMAN	26	160790	1	1	1	1	0.03	Isoform 2 of Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9
115	1	Human_Uniprot_2018	sp|A0A0A0MS15|HV349_HUMAN	25	13219	1	1	1	1	0.42	Immunoglobulin heavy variable 3-49 OS=Homo sapiens OX=9606 GN=IGHV3-49 PE=3 SV=1
116	1	Human_Uniprot_2018	sp|P07360|CO8G_HUMAN	25	22435	1	1	1	1	0.23	Complement component C8 gamma chain OS=Homo sapiens OX=9606 GN=C8G PE=1 SV=3
117	1	Human_Uniprot_2018	sp|Q9ULH7-4|MKL2_HUMAN	25	114220	1	1	1	1	0.04	Isoform 4 of MKL/myocardin-like protein 2 OS=Homo sapiens OX=9606 GN=MKL2
118	1	Human_Uniprot_2018	tr|F5GZG1|F5GZG1_HUMAN	23	13937	1	1	1	1	0.39	Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=8
119	1	Human_Uniprot_2018	tr|H3BPS8|H3BPS8_HUMAN	23	30693	1	1	1	1	0.16	Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=1
120	1	Human_Uniprot_2018	sp|A0A0B4J1Y9|HV372_HUMAN	23	13366	1	1	1	1	0.42	Immunoglobulin heavy variable 3-72 OS=Homo sapiens OX=9606 GN=IGHV3-72 PE=3 SV=1
121	1	Human_Uniprot_2018	sp|P01742|HV169_HUMAN	22	12765	1	1	1	1	0.44	Immunoglobulin heavy variable 1-69 OS=Homo sapiens OX=9606 GN=IGHV1-69 PE=1 SV=2
122	1	Human_Uniprot_2018	tr|X6RJP6|X6RJP6_HUMAN	22	21244	1	1	1	1	0.25	Transgelin-2 (Fragment) OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=1

WITH PAS - DAY 7 3(a)											
Family	**Member**	**Database**	**Accession**	**Score**	**Mass**	**Num. of matches**	**Num. of significant matches**	**Num. of sequences**	**Num. of significant sequences**	**emPAI**	**Description**
1	1	Human_Uniprot_2018	sp|P02768|ALBU_HUMAN	6786	71317	314	314	25	25	4.95	Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2
2	1	Human_Uniprot_2018	sp|P01024|CO3_HUMAN	3965	188569	154	154	48	48	2.32	Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2
3	1	Human_Uniprot_2018	sp|P01023|A2MG_HUMAN	3080	164613	118	118	38	38	1.97	Alpha-2-macroglobulin OS=Homo sapiens OX=9606 GN=A2M PE=1 SV=3
4	1	Human_Uniprot_2018	sp|P02787|TRFE_HUMAN	2428	79294	111	111	17	17	2.09	Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=3
5	1	Human_Uniprot_2018	sp|P01834|IGKC_HUMAN	2292	11929	88	88	6	6	9.3	Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2
6	1	Human_Uniprot_2018	sp|P04114|APOB_HUMAN	2249	516651	115	115	74	74	0.97	Apolipoprotein B-100 OS=Homo sapiens OX=9606 GN=APOB PE=1 SV=2
7	1	Human_Uniprot_2018	sp|P01009|A1AT_HUMAN	2148	46878	85	85	18	18	5.08	Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3
8	1	Human_Uniprot_2018	sp|P02647|APOA1_HUMAN	1857	30759	69	69	21	21	23.46	Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1
9	1	Human_Uniprot_2018	sp|P02675|FIBB_HUMAN	1741	56577	73	73	19	19	3.84	Fibrinogen beta chain OS=Homo sapiens OX=9606 GN=FGB PE=1 SV=2
10	1	Human_Uniprot_2018	tr|A0A0A0MS08|A0A0A0MS08_HUMAN	1714	44511	73	73	6	6	0.88	Immunoglobulin heavy constant gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1
10	2	Human_Uniprot_2018	sp|P01861|IGHG4_HUMAN	872	36431	29	29	5	5	0.9	Immunoglobulin heavy constant gamma 4 OS=Homo sapiens OX=9606 GN=IGHG4 PE=1 SV=1
10	3	Human_Uniprot_2018	sp|P01860|IGHG3_HUMAN	606	42287	31	31	4	4	0.56	Immunoglobulin heavy constant gamma 3 OS=Homo sapiens OX=9606 GN=IGHG3 PE=1 SV=2
10	4	Human_Uniprot_2018	sp|P01859|IGHG2_HUMAN	570	36505	30	30	3	3	0.67	Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=2
11	1	Human_Uniprot_2018	tr|A0A0G2JL54|A0A0G2JL54_HUMAN	1618	189080	56	56	26	26	0.91	Complement C4-B OS=Homo sapiens OX=9606 GN=C4B_2 PE=1 SV=1
11	2	Human_Uniprot_2018	tr|A0A0G2JPR0|A0A0G2JPR0_HUMAN	1508	194351	55	55	26	26	0.88	Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=1
12	1	Human_Uniprot_2018	sp|P02671-2|FIBA_HUMAN	1487	70227	65	65	14	14	1.73	Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA
13	1	Human_Uniprot_2018	sp|P02766|TTHY_HUMAN	1193	15991	45	45	10	10	17.26	Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1
14	1	Human_Uniprot_2018	sp|P00450|CERU_HUMAN	859	122983	44	44	17	17	0.92	Ceruloplasmin OS=Homo sapiens OX=9606 GN=CP PE=1 SV=1
14	2	Human_Uniprot_2018	tr|E9PFZ2|E9PFZ2_HUMAN	671	109493	37	37	16	16	0.99	Ceruloplasmin OS=Homo sapiens OX=9606 GN=CP PE=1 SV=1
15	1	Human_Uniprot_2018	sp|P02751-10|FINC_HUMAN	858	243068	35	35	20	20	0.47	Isoform 10 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1
16	1	Human_Uniprot_2018	tr|B7ZKJ8|B7ZKJ8_HUMAN	838	104044	41	41	19	19	1.36	ITIH4 protein OS=Homo sapiens OX=9606 GN=ITIH4 PE=1 SV=1
17	1	Human_Uniprot_2018	tr|C9JC84|C9JC84_HUMAN	778	52932	36	36	11	11	1.9	Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=1
18	1	Human_Uniprot_2018	tr|A0A1B0GUU9|A0A1B0GUU9_HUMAN	740	52518	31	31	8	8	1.05	Immunoglobulin heavy constant mu (Fragment) OS=Homo sapiens OX=9606 GN=IGHM PE=1 SV=1
19	1	Human_Uniprot_2018	sp|A0M8Q6|IGLC7_HUMAN	688	11418	24	24	3	3	2.35	Immunoglobulin lambda constant 7 OS=Homo sapiens OX=9606 GN=IGLC7 PE=1 SV=3
19	2	Human_Uniprot_2018	sp|B9A064|IGLL5_HUMAN	419	23391	19	19	4	4	1.22	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens OX=9606 GN=IGLL5 PE=2 SV=2
20	1	Human_Uniprot_2018	sp|P19827|ITIH1_HUMAN	671	101782	21	21	10	10	0.59	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens OX=9606 GN=ITIH1 PE=1 SV=3
21	1	Human_Uniprot_2018	sp|P01011|AACT_HUMAN	665	47792	22	22	11	11	1.94	Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=2
22	1	Human_Uniprot_2018	tr|A0A286YEY1|A0A286YEY1_HUMAN	649	43620	15	15	2	2	0.24	Immunoglobulin heavy constant alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=1
22	2	Human_Uniprot_2018	tr|A0A0G2JMB2|A0A0G2JMB2_HUMAN	565	37283	14	14	2	2	0.29	Immunoglobulin heavy constant alpha 2 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA2 PE=1 SV=1
23	1	Human_Uniprot_2018	sp|P01619|KV320_HUMAN	553	12663	11	11	3	3	1.99	Immunoglobulin kappa variable 3-20 OS=Homo sapiens OX=9606 GN=IGKV3-20 PE=1 SV=2
24	1	Human_Uniprot_2018	tr|D6RF35|D6RF35_HUMAN	546	54583	23	23	6	6	0.68	Vitamin D-binding protein OS=Homo sapiens OX=9606 GN=GC PE=1 SV=1
25	1	Human_Uniprot_2018	tr|A0A2R8Y793|A0A2R8Y793_HUMAN	529	34405	23	23	8	8	1.97	Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1
25	2	Human_Uniprot_2018	sp|P68032|ACTC_HUMAN	267	42334	16	16	5	5	0.74	Actin, alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1
26	1	Human_Uniprot_2018	sp|P01008|ANT3_HUMAN	517	53025	28	28	13	13	2.16	Antithrombin-III OS=Homo sapiens OX=9606 GN=SERPINC1 PE=1 SV=1
27	1	Human_Uniprot_2018	sp|P68871|HBB_HUMAN	486	16102	14	14	6	6	4.65	Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2
28	1	Human_Uniprot_2018	sp|P02790|HEMO_HUMAN	438	52385	23	23	7	7	0.87	Hemopexin OS=Homo sapiens OX=9606 GN=HPX PE=1 SV=2
29	1	Human_Uniprot_2018	sp|P04264|K2C1_HUMAN	428	66170	16	16	10	10	1.04	Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6
29	2	Human_Uniprot_2018	sp|P35908|K22E_HUMAN	95	65678	3	3	3	3	0.24	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2
30	1	Human_Uniprot_2018	tr|Q5T985|Q5T985_HUMAN	427	105606	24	24	11	11	0.63	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens OX=9606 GN=ITIH2 PE=1 SV=1
31	1	Human_Uniprot_2018	sp|P13645|K1C10_HUMAN	395	59020	13	13	7	7	0.75	Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6
32	1	Human_Uniprot_2018	tr|J3QLC9|J3QLC9_HUMAN	382	41381	14	14	5	5	0.76	Haptoglobin (Fragment) OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1
33	1	Human_Uniprot_2018	tr|A0A2Q2TTZ9|A0A2Q2TTZ9_HUMAN	374	11949	5	5	2	2	1.16	Immunoglobulin kappa variable 1-33 OS=Homo sapiens OX=9606 GN=IGKV1D-33 PE=1 SV=1
34	1	Human_Uniprot_2018	sp|P06727|APOA4_HUMAN	365	45371	17	17	8	8	1.29	Apolipoprotein A-IV OS=Homo sapiens OX=9606 GN=APOA4 PE=1 SV=3
35	1	Human_Uniprot_2018	sp|P04196|HRG_HUMAN	334	60510	14	14	5	5	0.47	Histidine-rich glycoprotein OS=Homo sapiens OX=9606 GN=HRG PE=1 SV=1

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
36	1	Human_Uniprot_2018	tr|A0A0A0MS51|A0A0A0MS51_HUMAN	332	82759	15	15	9	9	0.67	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
37	1	Human_Uniprot_2018	sp|P01019|ANGT_HUMAN	302	53406	12	12	7	7	0.85	Angiotensinogen OS=Homo sapiens OX=9606 GN=AGT PE=1 SV=1
38	1	Human_Uniprot_2018	tr|E9PIT3|E9PIT3_HUMAN	286	66792	9	9	4	4	0.33	Prothrombin OS=Homo sapiens OX=9606 GN=F2 PE=1 SV=1
39	1	Human_Uniprot_2018	sp|P02649|APOE_HUMAN	279	36246	11	11	6	6	1.17	Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1
40	1	Human_Uniprot_2018	sp|P02763|A1AG1_HUMAN	275	23725	17	17	4	4	1.19	Alpha-1-acid glycoprotein 1 OS=Homo sapiens OX=9606 GN=ORM1 PE=1 SV=1
40	2	Human_Uniprot_2018	sp|P19652|A1AG2_HUMAN	115	23873	8	8	3	3	0.8	Alpha-1-acid glycoprotein 2 OS=Homo sapiens OX=9606 GN=ORM2 PE=1 SV=2
41	1	Human_Uniprot_2018	sp|P04004|VTNC_HUMAN	272	55069	9	9	3	3	0.29	Vitronectin OS=Homo sapiens OX=9606 GN=VTN PE=1 SV=1
42	1	Human_Uniprot_2018	sp|P05155-2|IC1_HUMAN	266	49954	10	10	7	7	0.93	Isoform 2 of Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1
43	1	Human_Uniprot_2018	sp|Q9Y490|TLN1_HUMAN	266	271766	13	13	11	11	0.21	Talin-1 OS=Homo sapiens OX=9606 GN=TLN1 PE=1 SV=3
44	1	Human_Uniprot_2018	sp|P25311|ZA2G_HUMAN	262	34465	7	7	4	4	0.72	Zinc-alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=AZGP1 PE=1 SV=2
45	1	Human_Uniprot_2018	sp|P01597|KV139_HUMAN	258	12900	6	6	2	2	1.05	Immunoglobulin kappa variable 1-39 OS=Homo sapiens OX=9606 GN=IGKV1-39 PE=1 SV=2
46	1	Human_Uniprot_2018	sp|P27169|PON1_HUMAN	252	39877	7	7	5	5	0.8	Serum paraoxonase/arylesterase 1 OS=Homo sapiens OX=9606 GN=PON1 PE=1 SV=3
47	1	Human_Uniprot_2018	tr|B4E1Z4|B4E1Z4_HUMAN	251	143191	10	10	5	5	0.18	cDNA FLJ55673, highly similar to Complement factor B (EC 3.4.21.47) OS=Homo sapiens OX=9606 PE=1 SV=1
48	1	Human_Uniprot_2018	sp|P04217|A1BG_HUMAN	248	54790	12	12	7	7	0.82	Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=4
49	1	Human_Uniprot_2018	sp|P08603|CFAH_HUMAN	245	143680	12	12	5	5	0.18	Complement factor H OS=Homo sapiens OX=9606 GN=CFH PE=1 SV=4
50	1	Human_Uniprot_2018	sp|A0A075B6K5|LV39_HUMAN	242	12438	2	2	1	1	0.45	Immunoglobulin lambda variable 3-9 OS=Homo sapiens OX=9606 GN=IGLV3-9 PE=3 SV=1
51	1	Human_Uniprot_2018	tr|B0YIW2|B0YIW2_HUMAN	242	12864	4	4	2	2	1.05	Apolipoprotein C-III variant 1 OS=Homo sapiens OX=9606 GN=APOC3 PE=1 SV=1
52	1	Human_Uniprot_2018	tr|A0A0G2JPA8|A0A0G2JPA8_HUMAN	238	48135	10	10	4	4	0.48	Alpha-2-antiplasmin OS=Homo sapiens OX=9606 GN=SERPINF2 PE=1 SV=1
53	1	Human_Uniprot_2018	tr|A0A0B4J2B5|A0A0B4J2B5_HUMAN	221	10764	10	10	2	2	1.35	Immunoglobulin heavy variable 3/OR16-9 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV3OR16-9 PE=1 SV=1
54	1	Human_Uniprot_2018	tr|C9JV77|C9JV77_HUMAN	217	40185	6	6	1	1	0.26	Alpha-2-HS-glycoprotein OS=Homo sapiens OX=9606 GN=AHSG PE=1 SV=1
55	1	Human_Uniprot_2018	sp|P10909-2|CLUS_HUMAN	214	58537	9	9	4	4	0.38	Isoform 2 of Clusterin OS=Homo sapiens OX=9606 GN=CLU
56	1	Human_Uniprot_2018	sp|P43652|AFAM_HUMAN	198	70963	12	12	5	5	0.39	Afamin OS=Homo sapiens OX=9606 GN=AFM PE=1 SV=1
57	1	Human_Uniprot_2018	sp|P35527|K1C9_HUMAN	163	62255	11	11	7	7	0.7	Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=3
58	1	Human_Uniprot_2018	sp|P35579|MYH9_HUMAN	155	227646	11	11	8	8	0.18	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4
59	1	Human_Uniprot_2018	sp|P01042-2|KNG1_HUMAN	142	48936	7	7	4	4	0.47	Isoform LMW of Kininogen-1 OS=Homo sapiens OX=9606 GN=KNG1
60	1	Human_Uniprot_2018	sp|A0A0C4DH38|HV551_HUMAN	130	12837	6	6	3	3	1.94	Immunoglobulin heavy variable 5-51 OS=Homo sapiens OX=9606 GN=IGHV5-51 PE=3 SV=1
61	1	Human_Uniprot_2018	tr|A0A024R0T9|A0A024R0T9_HUMAN	122	11277	6	6	3	3	2.39	Apolipoprotein C-II isoform 1 OS=Homo sapiens OX=9606 GN=APOC4-APOC2 PE=1 SV=1
62	1	Human_Uniprot_2018	tr|A0A0A0MSV6|A0A0A0MSV6_HUMAN	120	24243	4	4	3	3	0.78	Complement C1q subcomponent subunit B (Fragment) OS=Homo sapiens OX=9606 GN=C1QB PE=1 SV=6
63	1	Human_Uniprot_2018	tr|A0A2R8Y7C0|A0A2R8Y7C0_HUMAN	116	13945	9	9	4	4	2.76	Hemoglobin subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1
64	1	Human_Uniprot_2018	tr|A0A0J9YY99|A0A0J9YY99_HUMAN	115	13128	5	5	2	2	1.03	Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1
65	1	Human_Uniprot_2018	sp|P02748|CO9_HUMAN	113	64615	5	5	3	3	0.24	Complement component C9 OS=Homo sapiens OX=9606 GN=C9 PE=1 SV=2
66	1	Human_Uniprot_2018	sp|A0A075B6S5|KV127_HUMAN	111	12874	3	3	1	1	0.43	Immunoglobulin kappa variable 1-27 OS=Homo sapiens OX=9606 GN=IGKV1-27 PE=3 SV=1
67	1	Human_Uniprot_2018	sp|P02775|CXCL7_HUMAN	110	14171	4	4	3	3	1.66	Platelet basic protein OS=Homo sapiens OX=9606 GN=PPBP PE=1 SV=3
68	1	Human_Uniprot_2018	tr|Q5VY30|Q5VY30_HUMAN	109	23301	4	4	2	2	0.49	Retinol-binding protein OS=Homo sapiens OX=9606 GN=RBP4 PE=1 SV=2
69	1	Human_Uniprot_2018	sp|P07737|PROF1_HUMAN	105	15216	7	7	4	4	2.39	Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2
70	1	Human_Uniprot_2018	sp|P02743|SAMP_HUMAN	105	25485	5	5	3	3	0.73	Serum amyloid P-component OS=Homo sapiens OX=9606 GN=APCS PE=1 SV=2
71	1	Human_Uniprot_2018	tr|V9GYE3|V9GYE3_HUMAN	102	5873	4	4	2	2	3.63	Apolipoprotein A-II OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1
72	1	Human_Uniprot_2018	tr|H9KV75|H9KV75_HUMAN	102	95279	6	6	5	5	0.28	Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1
73	1	Human_Uniprot_2018	sp|P07360|CO8G_HUMAN	98	22435	5	5	3	3	0.87	Complement component C8 gamma chain OS=Homo sapiens OX=9606 GN=C8G PE=1 SV=3
74	1	Human_Uniprot_2018	sp|P01599|KV117_HUMAN	92	12941	2	2	2	2	1.04	Immunoglobulin kappa variable 1-17 OS=Homo sapiens OX=9606 GN=IGKV1-17 PE=1 SV=2
75	1	Human_Uniprot_2018	tr|A0A087WWY3|A0A087WWY3_HUMAN	92	248149	9	9	8	8	0.16	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=1
76	1	Human_Uniprot_2018	sp|P01700|LV147_HUMAN	90	12447	2	2	1	1	0.45	Immunoglobulin lambda variable 1-47 OS=Homo sapiens OX=9606 GN=IGLV1-47 PE=1 SV=2
77	1	Human_Uniprot_2018	sp|P04003|C4BPA_HUMAN	90	69042	6	6	4	4	0.31	C4b-binding protein alpha chain OS=Homo sapiens OX=9606 GN=C4BPA PE=1 SV=2
78	1	Human_Uniprot_2018	sp|Q9H4B7|TBB1_HUMAN	90	50865	4	4	2	2	0.2	Tubulin beta-1 chain OS=Homo sapiens OX=9606 GN=TUBB1 PE=1 SV=1
78	2	Human_Uniprot_2018	sp|P07437|TBB5_HUMAN	80	50095	4	4	3	3	0.33	Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2
79	1	Human_Uniprot_2018	tr|X6RJP6|X6RJP6_HUMAN	83	21244	4	4	3	3	0.93	Transgelin-2 (Fragment) OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=1

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
80	1	Human_Uniprot_2018	tr|F5GZG1|F5GZG1_HUMAN	82	13937	2	2	1	1	0.39	Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=8
81	1	Human_Uniprot_2018	sp|P01721|LV657_HUMAN	81	12729	1	1	1	1	0.44	Immunoglobulin lambda variable 6-57 OS=Homo sapiens OX=9606 GN=IGLV6-57 PE=1 SV=2
82	1	Human_Uniprot_2018	tr|K7ERI9|K7ERI9_HUMAN	77	8642	6	6	2	2	1.88	Apolipoprotein C-I (Fragment) OS=Homo sapiens OX=9606 GN=APOC1 PE=1 SV=1
83	1	Human_Uniprot_2018	sp|P06702|S10A9_HUMAN	72	13291	2	2	1	1	0.42	Protein S100-A9 OS=Homo sapiens OX=9606 GN=S100A9 PE=1 SV=1
84	1	Human_Uniprot_2018	sp|P02750|A2GL_HUMAN	71	38382	7	7	4	4	0.63	Leucine-rich alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=LRG1 PE=1 SV=2
85	1	Human_Uniprot_2018	sp|P13671|CO6_HUMAN	70	108367	2	2	1	1	0.04	Complement component C6 OS=Homo sapiens OX=9606 GN=C6 PE=1 SV=3
86	1	Human_Uniprot_2018	sp|P62328|TYB4_HUMAN	68	5050	2	2	1	1	1.45	Thymosin beta-4 OS=Homo sapiens OX=9606 GN=TMSB4X PE=1 SV=2
87	1	Human_Uniprot_2018	sp|A0A0C4DH68|KV224_HUMAN	66	13185	1	1	1	1	0.42	Immunoglobulin kappa variable 2-24 OS=Homo sapiens OX=9606 GN=IGKV2-24 PE=3 SV=1
88	1	Human_Uniprot_2018	tr|S4R3Y4|S4R3Y4_HUMAN	66	26683	1	1	1	1	0.19	Protein AMBP OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1
89	1	Human_Uniprot_2018	sp|P51884|LUM_HUMAN	65	38747	3	3	3	3	0.44	Lumican OS=Homo sapiens OX=9606 GN=LUM PE=1 SV=2
90	1	Human_Uniprot_2018	sp|P08185|CBG_HUMAN	64	45283	1	1	1	1	0.11	Corticosteroid-binding globulin OS=Homo sapiens OX=9606 GN=SERPINA6 PE=1 SV=1
91	1	Human_Uniprot_2018	tr|A0A2R8Y3M9|A0A2R8Y3M9_HUMAN	63	74186	3	3	2	2	0.14	Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1
92	1	Human_Uniprot_2018	tr|B4DPQ0|B4DPQ0_HUMAN	61	83376	3	3	3	3	0.18	cDNA FLJ54471, highly similar to Complement C1r subcomponent (EC 3.4.21.41) OS=Homo sapiens OX=9606 GN=C1R PE=1 SV=1
93	1	Human_Uniprot_2018	sp|Q96PD5-2|PGRP2_HUMAN	61	68699	6	6	5	5	0.41	Isoform 2 of N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens OX=9606 GN=PGLYRP2
94	1	Human_Uniprot_2018	sp|A0A0C4DH31|HV118_HUMAN	58	12926	2	2	1	1	0.43	Immunoglobulin heavy variable 1-18 OS=Homo sapiens OX=9606 GN=IGHV1-18 PE=3 SV=1
95	1	Human_Uniprot_2018	sp|A0A0J9YX35|HV64D_HUMAN	56	12985	2	2	1	1	0.43	Immunoglobulin heavy variable 3-64D OS=Homo sapiens OX=9606 GN=IGHV3-64D PE=3 SV=1
96	1	Human_Uniprot_2018	tr|Q5SRP5|Q5SRP5_HUMAN	54	14404	2	2	1	1	0.38	Apolipoprotein M OS=Homo sapiens OX=9606 GN=APOM PE=1 SV=1
97	1	Human_Uniprot_2018	sp|P02747|C1QC_HUMAN	54	25985	1	1	1	1	0.2	Complement C1q subcomponent subunit C OS=Homo sapiens OX=9606 GN=C1QC PE=1 SV=3
98	1	Human_Uniprot_2018	sp|P36955|PEDF_HUMAN	52	46454	3	3	3	3	0.35	Pigment epithelium-derived factor OS=Homo sapiens OX=9606 GN=SERPINF1 PE=1 SV=4
99	1	Human_Uniprot_2018	sp|P07996|TSP1_HUMAN	50	133291	3	3	3	3	0.11	Thrombospondin-1 OS=Homo sapiens OX=9606 GN=THBS1 PE=1 SV=2
100	1	Human_Uniprot_2018	sp|P18206-2|VINC_HUMAN	48	117220	5	5	3	3	0.13	Isoform 1 of Vinculin OS=Homo sapiens OX=9606 GN=VCL
101	1	Human_Uniprot_2018	tr|Q5H928|Q5H928_HUMAN	48	17498	3	3	1	1	0.3	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=1
102	1	Human_Uniprot_2018	sp|P00748|FA12_HUMAN	48	70029	2	2	1	1	0.07	Coagulation factor XII OS=Homo sapiens OX=9606 GN=F12 PE=1 SV=3
103	1	Human_Uniprot_2018	sp|P35858-2|ALS_HUMAN	47	70990	4	4	4	4	0.3	Isoform 2 of Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens OX=9606 GN=IGFALS
104	1	Human_Uniprot_2018	sp|A0A0B4J1Y9|HV372_HUMAN	46	13366	1	1	1	1	0.42	Immunoglobulin heavy variable 3-72 OS=Homo sapiens OX=9606 GN=IGHV3-72 PE=3 SV=1
105	1	Human_Uniprot_2018	sp|P00747|PLMN_HUMAN	45	93247	3	3	2	2	0.11	Plasminogen OS=Homo sapiens OX=9606 GN=PLG PE=1 SV=2
106	1	Human_Uniprot_2018	sp|P43251-2|BTD_HUMAN	44	62383	1	1	1	1	0.08	Isoform 2 of Biotinidase OS=Homo sapiens OX=9606 GN=BTD
107	1	Human_Uniprot_2018	sp|P05546|HEP2_HUMAN	43	57205	2	2	2	2	0.18	Heparin cofactor 2 OS=Homo sapiens OX=9606 GN=SERPIND1 PE=1 SV=3
108	1	Human_Uniprot_2018	tr|A0A087X232|A0A087X232_HUMAN	41	77396	2	2	1	1	0.06	Complement C1s subcomponent OS=Homo sapiens OX=9606 GN=C1S PE=1 SV=1
109	1	Human_Uniprot_2018	tr|A0A0C4DH36|A0A0C4DH36_HUMAN	40	12921	1	1	1	1	0.43	Immunoglobulin heavy variable 3-38 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV3-38 PE=1 SV=1
110	1	Human_Uniprot_2018	tr|F5H5D3|F5H5D3_HUMAN	40	58606	1	1	1	1	0.08	Tubulin alpha chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1
111	1	Human_Uniprot_2018	sp|P15814|IGLL1_HUMAN	40	23177	2	2	1	1	0.22	Immunoglobulin lambda-like polypeptide 1 OS=Homo sapiens OX=9606 GN=IGLL1 PE=1 SV=1
112	1	Human_Uniprot_2018	tr|C9JF17|C9JF17_HUMAN	39	24541	2	2	2	2	0.46	Apolipoprotein D (Fragment) OS=Homo sapiens OX=9606 GN=APOD PE=1 SV=1
113	1	Human_Uniprot_2018	sp|P08514-2|ITA2B_HUMAN	39	110645	3	3	3	3	0.14	Isoform 2 of Integrin alpha-IIb OS=Homo sapiens OX=9606 GN=ITGA2B
114	1	Human_Uniprot_2018	sp|P06312|KV401_HUMAN	38	13486	1	1	1	1	0.41	Immunoglobulin kappa variable 4-1 OS=Homo sapiens OX=9606 GN=IGKV4-1 PE=1 SV=1
115	1	Human_Uniprot_2018	tr|E9PHK0|E9PHK0_HUMAN	34	18125	1	1	1	1	0.29	Tetranectin OS=Homo sapiens OX=9606 GN=CLEC3B PE=1 SV=1
116	1	Human_Uniprot_2018	tr|A0A075B6Z2|A0A075B6Z2_HUMAN	34	2220	2	2	1	1	5.73	T cell receptor alpha joining 56 (Fragment) OS=Homo sapiens OX=9606 GN=TRAJ56 PE=4 SV=1
117	1	Human_Uniprot_2018	tr|K7EJY8|K7EJY8_HUMAN	34	16000	1	1	1	1	0.34	Galectin-3-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1
118	1	Human_Uniprot_2018	tr|H0YAC1|H0YAC1_HUMAN	33	79001	1	1	1	1	0.06	Plasma kallikrein (Fragment) OS=Homo sapiens OX=9606 GN=KLKB1 PE=1 SV=1
119	1	Human_Uniprot_2018	tr|F5H1C6|F5H1C6_HUMAN	31	33292	1	1	1	1	0.15	Fermitin family homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=FERMT3 PE=1 SV=1
120	1	Human_Uniprot_2018	sp|P10643|CO7_HUMAN	31	96650	1	1	1	1	0.05	Complement component C7 OS=Homo sapiens OX=9606 GN=C7 PE=1 SV=2

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
121	1	Human_Uniprot_2018	tr|A0A096LPE2|A0A096LPE2_HUMAN	30	23510	1	1	1	1	0.22	SAA2-SAA4 readthrough OS=Homo sapiens OX=9606 GN=SAA2-SAA4 PE=4 SV=1
122	1	Human_Uniprot_2018	sp|A0A0C4DH29|HV103_HUMAN	30	13113	1	1	1	1	0.42	Immunoglobulin heavy variable 1-3 OS=Homo sapiens OX=9606 GN=IGHV1-3 PE=3 SV=1
123	1	Human_Uniprot_2018	sp|P22792|CPN2_HUMAN	30	61373	2	2	2	2	0.17	Carboxypeptidase N subunit 2 OS=Homo sapiens OX=9606 GN=CPN2 PE=1 SV=3
124	1	Human_Uniprot_2018	sp|P01602|KV105_HUMAN	29	12944	1	1	1	1	0.43	Immunoglobulin kappa variable 1-5 OS=Homo sapiens OX=9606 GN=IGKV1-5 PE=1 SV=2
125	1	Human_Uniprot_2018	sp|A0A075B6P5|KV228_HUMAN	28	13062	1	1	1	1	0.42	Immunoglobulin kappa variable 2-28 OS=Homo sapiens OX=9606 GN=IGKV2-28 PE=3 SV=1
126	1	Human_Uniprot_2018	sp|P08567|PLEK_HUMAN	28	40499	3	3	3	3	0.42	Pleckstrin OS=Homo sapiens OX=9606 GN=PLEK PE=1 SV=3
127	1	Human_Uniprot_2018	tr|A0A087X1J7|A0A087X1J7_HUMAN	28	25614	1	1	1	1	0.2	Glutathione peroxidase OS=Homo sapiens OX=9606 GN=GPX3 PE=1 SV=1
128	1	Human_Uniprot_2018	tr|F5GY80|F5GY80_HUMAN	27	61485	1	1	1	1	0.08	Complement component C8 beta chain OS=Homo sapiens OX=9606 GN=C8B PE=1 SV=1
129	1	Human_Uniprot_2018	sp|P23142|FBLN1_HUMAN	27	81268	1	1	1	1	0.06	Fibulin-1 OS=Homo sapiens OX=9606 GN=FBLN1 PE=1 SV=4
130	1	Human_Uniprot_2018	sp|Q7Z2Y8|GVIN1_HUMAN	27	281950	2	2	1	1	0.02	Interferon-induced very large GTPase 1 OS=Homo sapiens OX=9606 GN=GVINP1 PE=2 SV=2
131	1	Human_Uniprot_2018	sp|P23083|HV102_HUMAN	26	13190	2	2	1	1	0.42	Immunoglobulin heavy variable 1-2 OS=Homo sapiens OX=9606 GN=IGHV1-2 PE=1 SV=2
132	1	Human_Uniprot_2018	tr|A8K7Q2|A8K7Q2_HUMAN	26	45481	1	1	1	1	0.11	Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1
133	1	Human_Uniprot_2018	tr|G5E9F8|G5E9F8_HUMAN	26	61914	2	2	1	1	0.08	Protein S (Alpha), isoform CRA_b OS=Homo sapiens OX=9606 GN=PROS1 PE=1 SV=1
134	1	Human_Uniprot_2018	sp|P27797|CALR_HUMAN	25	48283	1	1	1	1	0.1	Calreticulin OS=Homo sapiens OX=9606 GN=CALR PE=1 SV=1
135	1	Human_Uniprot_2018	sp|P02745|C1QA_HUMAN	25	26285	1	1	1	1	0.19	Complement C1q subcomponent subunit A OS=Homo sapiens OX=9606 GN=C1QA PE=1 SV=2
136	1	Human_Uniprot_2018	tr|A0A0U1RRK8|A0A0U1RRK8_HUMAN	25	51262	1	1	1	1	0.1	Sickle tail protein homolog (Fragment) OS=Homo sapiens OX=9606 GN=KIAA1217 PE=1 SV=1
137	1	Human_Uniprot_2018	sp|P01031|CO5_HUMAN	25	189897	1	1	1	1	0.03	Complement C5 OS=Homo sapiens OX=9606 GN=C5 PE=1 SV=4
138	1	Human_Uniprot_2018	tr|A0A087WY61|A0A087WY61_HUMAN	24	237388	1	1	1	1	0.02	Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 PE=1 SV=1
139	1	Human_Uniprot_2018	tr|H0YM60|H0YM60_HUMAN	24	4288	1	1	1	1	1.79	H/ACA ribonucleoprotein complex subunit 3 OS=Homo sapiens OX=9606 GN=NOP10 PE=1 SV=1
140	1	Human_Uniprot_2018	sp|A0A0A0MS15|HV349_HUMAN	23	13219	1	1	1	1	0.42	Immunoglobulin heavy variable 3-49 OS=Homo sapiens OX=9606 GN=IGHV3-49 PE=3 SV=1
141	1	Human_Uniprot_2018	sp|Q9Y4E5-2|ZN451_HUMAN	23	118552	1	1	1	1	0.04	Isoform 2 of E3 SUMO-protein ligase ZNF451 OS=Homo sapiens OX=9606 GN=ZNF451
142	1	Human_Uniprot_2018	tr|D6RD66|D6RD66_HUMAN	23	27066	1	1	1	1	0.19	WD repeat-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=WDR1 PE=1 SV=1
143	1	Human_Uniprot_2018	sp|P01742|HV169_HUMAN	22	12765	2	2	2	2	1.06	Immunoglobulin heavy variable 1-69 OS=Homo sapiens OX=9606 GN=IGHV1-69 PE=1 SV=2
144	1	Human_Uniprot_2018	sp|A0A0A0MRZ8|KVD11_HUMAN	22	12731	1	1	1	1	0.44	Immunoglobulin kappa variable 3D-11 OS=Homo sapiens OX=9606 GN=IGKV3D-11 PE=3 SV=6
145	1	Human_Uniprot_2018	sp|Q96GE9|DMAC1_HUMAN	22	12363	1	1	1	1	0.45	Distal membrane-arm assembly complex protein 1 OS=Homo sapiens OX=9606 GN=DMAC1 PE=1 SV=1
146	1	Human_Uniprot_2018	sp|P78383|S35B1_HUMAN	22	36135	1	1	1	1	0.14	Solute carrier family 35 member B1 OS=Homo sapiens OX=9606 GN=SLC35B1 PE=1 SV=1
147	1	Human_Uniprot_2018	tr|H3BQ34|H3BQ34_HUMAN	21	30929	1	1	1	1	0.16	Pyruvate kinase OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1
148	1	Human_Uniprot_2018	sp|P05543|THBG_HUMAN	21	46637	1	1	1	1	0.11	Thyroxine-binding globulin OS=Homo sapiens OX=9606 GN=SERPINA7 PE=1 SV=2
149	1	Human_Uniprot_2018	sp|O75363|BCAS1_HUMAN	21	61957	1	1	1	1	0.08	Breast carcinoma-amplified sequence 1 OS=Homo sapiens OX=9606 GN=BCAS1 PE=1 SV=2
150	1	Human_Uniprot_2018	tr|H0YEH6|H0YEH6_HUMAN	20	17194	1	1	1	1	0.31	RING finger protein 121 (Fragment) OS=Homo sapiens OX=9606 GN=RNF121 PE=1 SV=1
151	1	Human_Uniprot_2018	tr|A0A2R8Y6X9|A0A2R8Y6X9_HUMAN	20	66793	1	1	1	1	0.07	V-type proton ATPase subunit a OS=Homo sapiens OX=9606 GN=ATP6V0A4 PE=1 SV=1
152	1	Human_Uniprot_2018	sp|Q92625|ANS1A_HUMAN	20	124001	1	1	1	1	0.04	Ankyrin repeat and SAM domain-containing protein 1A OS=Homo sapiens OX=9606 GN=ANKS1A PE=1 SV=4
153	1	Human_Uniprot_2018	sp|O94782|UBP1_HUMAN	20	89179	1	1	1	1	0.05	Ubiquitin carboxyl-terminal hydrolase 1 OS=Homo sapiens OX=9606 GN=USP1 PE=1 SV=1
154	1	Human_Uniprot_2018	tr|C9J1P0|C9J1P0_HUMAN	19	12907	1	1	1	1	0.43	Transmembrane protein 169 (Fragment) OS=Homo sapiens OX=9606 GN=TMEM169 PE=1 SV=1
155	1	Human_Uniprot_2018	tr|H0YEQ6|H0YEQ6_HUMAN	19	19068	1	1	1	1	0.28	COMM domain-containing protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=COMMD5 PE=1 SV=1

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
156	1	Human_Uniprot_2018	tr|A0A0A0MRA3|A0A0A0MRA3_HUMAN	19	3032754	1	1	1	1	0	Titin OS=Homo sapiens OX=9606 GN=TTN PE=1 SV=1
157	1	Human_Uniprot_2018	tr|H0YBF2|H0YBF2_HUMAN	18	15383	1	1	1	1	0.35	Matrilin-2 (Fragment) OS=Homo sapiens OX=9606 GN=MATN2 PE=1 SV=1
158	1	Human_Uniprot_2018	tr|A0A0A0MTG1|A0A0A0MTG1_HUMAN	18	119427	1	1	1	1	0.04	Valine--tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=VARS2 PE=1 SV=1
159	1	Human_Uniprot_2018	tr|A0A0C4DG07|A0A0C4DG07_HUMAN	18	76549	1	1	1	1	0.06	Nibrin OS=Homo sapiens OX=9606 GN=NBN PE=1 SV=1
160	1	Human_Uniprot_2018	sp|O75882-2|ATRN_HUMAN	18	146125	1	1	1	1	0.03	Isoform 2 of Attractin OS=Homo sapiens OX=9606 GN=ATRN
161	1	Human_Uniprot_2018	tr|H0Y6X7|H0Y6X7_HUMAN	18	23427	1	1	1	1	0.22	Nucleoporin-62 C-terminal-like protein (Fragment) OS=Homo sapiens OX=9606 GN=NUP62CL PE=4 SV=1
162	1	Human_Uniprot_2018	tr|J3KPH2|J3KPH2_HUMAN	18	99298	1	1	1	1	0.05	Arachidonate lipoxygenase 3, isoform CRA_a OS=Homo sapiens OX=9606 GN=ALOXE3 PE=1 SV=1

WITHOUT PAS - DAY 0 1(b)											
Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
1	1	Human_Uniprot_2018	sp|P02768|ALBU_HUMAN	9139	71317	409	409	22	22	3.57	Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2
2	1	Human_Uniprot_2018	sp|P01024|CO3_HUMAN	4964	188569	183	183	47	47	2.41	Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2
3	1	Human_Uniprot_2018	sp|P04114|APOB_HUMAN	3832	516651	179	179	88	88	1.23	Apolipoprotein B-100 OS=Homo sapiens OX=9606 GN=APOB PE=1 SV=2
4	1	Human_Uniprot_2018	sp|P01023|A2MG_HUMAN	3775	164613	161	161	38	38	1.97	Alpha-2-macroglobulin OS=Homo sapiens OX=9606 GN=A2M PE=1 SV=3
5	1	Human_Uniprot_2018	sp|P02787|TRFE_HUMAN	2607	79294	113	113	19	19	2.48	Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=3
6	1	Human_Uniprot_2018	sp|P01009|A1AT_HUMAN	2430	46878	86	86	16	16	3.97	Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3
7	1	Human_Uniprot_2018	sp|P02647|APOA1_HUMAN	2415	30759	97	97	21	21	27.48	Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1
8	1	Human_Uniprot_2018	sp|P01834|IGKC_HUMAN	2397	11929	85	85	6	6	9.3	Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2
9	1	Human_Uniprot_2018	tr|A0A0G2JL54|A0A0G2JL54_HUMAN	2345	189080	83	83	31	31	1.17	Complement C4-B OS=Homo sapiens OX=9606 GN=C4B_2 PE=1 SV=1
9	2	Human_Uniprot_2018	sp|P0C0L4-2|CO4A_HUMAN	2012	189125	76	76	30	30	1.11	Isoform 2 of Complement C4-A OS=Homo sapiens OX=9606 GN=C4A
10	1	Human_Uniprot_2018	sp|P02675|FIBB_HUMAN	2263	56577	88	88	20	20	4.26	Fibrinogen beta chain OS=Homo sapiens OX=9606 GN=FGB PE=1 SV=2
11	1	Human_Uniprot_2018	tr|A0A0A0MS08|A0A0A0MS08_HUMAN	2147	44511	86	86	8	8	1.32	Immunoglobulin heavy constant gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1
11	2	Human_Uniprot_2018	sp|P01861|IGHG4_HUMAN	1091	36431	35	35	6	6	1.17	Immunoglobulin heavy constant gamma 4 OS=Homo sapiens OX=9606 GN=IGHG4 PE=1 SV=1
11	3	Human_Uniprot_2018	sp|P01860|IGHG3_HUMAN	930	42287	49	49	5	5	0.74	Immunoglobulin heavy constant gamma 3 OS=Homo sapiens OX=9606 GN=IGHG3 PE=1 SV=2
11	4	Human_Uniprot_2018	sp|P01859|IGHG2_HUMAN	928	36505	52	52	4	4	0.9	Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=2
12	1	Human_Uniprot_2018	sp|P02671-2|FIBA_HUMAN	2075	70227	80	80	17	17	2.34	Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA
13	1	Human_Uniprot_2018	sp|P02766|TTHY_HUMAN	1298	15991	48	48	10	10	17.26	Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1
14	1	Human_Uniprot_2018	sp|P02751-10|FINC_HUMAN	1211	243068	47	47	22	22	0.53	Isoform 10 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1
15	1	Human_Uniprot_2018	sp|P00450|CERU_HUMAN	1057	122983	51	51	16	16	0.85	Cyclophilin A=Homo sapiens OX=9606 GN=CP PE=1 SV=1
16	1	Human_Uniprot_2018	tr|C9JC84|C9JC84_HUMAN	1013	52932	38	38	10	10	1.43	Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=1
17	1	Human_Uniprot_2018	tr|A0A1B0GUU9|A0A1B0GUU9_HUMAN	876	52518	35	35	8	8	1.05	Immunoglobulin heavy constant mu (Fragment) OS=Homo sapiens OX=9606 GN=IGHM PE=1 SV=1
18	1	Human_Uniprot_2018	tr|B7ZKJ8|B7ZKJ8_HUMAN	869	104044	38	38	16	16	1.06	ITIH4 protein OS=Homo sapiens OX=9606 GN=ITIH4 PE=1 SV=1
19	1	Human_Uniprot_2018	sp|A0M8Q6|IGLC7_HUMAN	765	11418	28	28	3	3	2.35	Immunoglobulin lambda constant 7 OS=Homo sapiens OX=9606 GN=IGLC7 PE=1 SV=3
19	2	Human_Uniprot_2018	sp|B9A064|IGLL5_HUMAN	621	23391	27	27	4	4	1.22	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens OX=9606 GN=IGLL5 PE=2 SV=2
20	1	Human_Uniprot_2018	sp|P01619|KV320_HUMAN	730	12663	12	12	2	2	1.08	Immunoglobulin kappa variable 3-20 OS=Homo sapiens OX=9606 GN=IGKV3-20 PE=1 SV=2
21	1	Human_Uniprot_2018	sp|P01011|AACT_HUMAN	702	47792	20	20	10	10	1.67	Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=2
22	1	Human_Uniprot_2018	tr|A0A286YEY1|A0A286YEY1_HUMAN	667	43620	18	18	3	3	0.38	Immunoglobulin heavy constant alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=1
22	2	Human_Uniprot_2018	tr|A0A0G2JMB2|A0A0G2JMB2_HUMAN	615	37283	17	17	3	3	0.46	Immunoglobulin heavy constant alpha 2 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA2 PE=1 SV=1
23	1	Human_Uniprot_2018	tr|A0A2R8Y793|A0A2R8Y793_HUMAN	621	34405	25	25	8	8	1.97	Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1
23	2	Human_Uniprot_2018	sp|P68032|ACTC_HUMAN	342	42334	18	18	6	6	0.95	Actin, alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1
24	1	Human_Uniprot_2018	sp|P19827|ITIH1_HUMAN	573	101782	23	23	10	10	0.59	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens OX=9606 GN=ITIH1 PE=1 SV=3
25	1	Human_Uniprot_2018	sp|P01008|ANT3_HUMAN	553	53025	26	26	11	11	1.65	Antithrombin-III OS=Homo sapiens OX=9606 GN=SERPINC1 PE=1 SV=1
26	1	Human_Uniprot_2018	sp|P06396|GELS_HUMAN	517	86043	23	23	11	11	0.83	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
27	1	Human_Uniprot_2018	sp|P01019|ANGT_HUMAN	514	53406	16	16	7	7	0.85	Angiotensinogen OS=Homo sapiens OX=9606 GN=AGT PE=1 SV=1
28	1	Human_Uniprot_2018	tr|D6RF35|D6RF35_HUMAN	496	54583	22	22	7	7	0.83	Vitamin D-binding protein OS=Homo sapiens OX=9606 GN=GC PE=1 SV=1
29	1	Human_Uniprot_2018	tr|E9PGN7|E9PGN7_HUMAN	470	59683	16	16	9	9	1.03	Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1 PE=1 SV=1
30	1	Human_Uniprot_2018	sp|P02790|HEMO_HUMAN	467	52385	29	29	9	9	1.24	Hemopexin OS=Homo sapiens OX=9606 GN=HPX PE=1 SV=2
31	1	Human_Uniprot_2018	sp|P68871|HBB_HUMAN	463	16102	14	14	6	6	4.65	Pleckstrin OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2
32	1	Human_Uniprot_2018	sp|P04196|HRG_HUMAN	427	60510	19	19	7	7	0.72	Histidine-rich glycoprotein OS=Homo sapiens OX=9606 GN=HRG PE=1 SV=1
33	1	Human_Uniprot_2018	sp|Q9Y490|TLN1_HUMAN	419	271766	20	20	15	15	0.3	Talin-1 OS=Homo sapiens OX=9606 GN=TLN1 PE=1 SV=3
34	1	Human_Uniprot_2018	tr|Q5T985|Q5T985_HUMAN	410	105606	20	20	10	10	0.56	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens OX=9606 GN=ITIH2 PE=1 SV=1
35	1	Human_Uniprot_2018	sp|P06727|APOA4_HUMAN	387	45371	19	19	9	9	1.54	Apolipoprotein A-IV OS=Homo sapiens OX=9606 GN=APOA4 PE=1 SV=3
36	1	Human_Uniprot_2018	sp|P02649|APOE_HUMAN	385	36246	12	12	7	7	1.47	Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1
37	1	Human_Uniprot_2018	tr|J3QLC9|J3QLC9_HUMAN	378	41381	17	17	6	6	0.97	Haptoglobin (Fragment) OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1
37	2	Human_Uniprot_2018	sp|P00739|HPTR_HUMAN	296	39518	11	11	4	4	0.61	RAP-1 OS=Homo sapiens OX=9606 GN=HPR PE=2 SV=2
38	1	Human_Uniprot_2018	tr|E9PIT3|E9PIT3_HUMAN	358	66792	15	15	4	4	0.33	Prothrombin OS=Homo sapiens OX=9606 GN=F2 PE=1 SV=1
39	1	Human_Uniprot_2018	sp|P04217|A1BG_HUMAN	340	54790	19	19	8	8	0.98	Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=4
40	1	Human_Uniprot_2018	tr|A0A2Q2TTZ9|A0A2Q2TTZ9_HUMAN	336	11949	7	7	2	2	1.16	Immunoglobulin kappa variable 1-33 OS=Homo sapiens OX=9606 GN=IGKV1D-33 PE=1 SV=1
41	1	Human_Uniprot_2018	sp|P04004|VTNC_HUMAN	307	55069	8	8	3	3	0.29	Vitronectin OS=Homo sapiens OX=9606 GN=VTN PE=1 SV=1
42	1	Human_Uniprot_2018	tr|A0A0B4J2B5|A0A0B4J2B5_HUMAN	299	10764	10	10	2	2	2.61	Immunoglobulin heavy variable 3/OR16-9 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV3OR16-9 PE=1 SV=1
43	1	Human_Uniprot_2018	sp|P02763|A1AG1_HUMAN	298	23725	14	14	3	3	0.8	Alpha-1-acid glycoprotein 1 OS=Homo sapiens OX=9606 GN=ORM1 PE=1 SV=1
43	2	Human_Uniprot_2018	sp|P19652|A1AG2_HUMAN	109	23873	6	6	2	2	0.48	Alpha-1-acid glycoprotein 2 OS=Homo sapiens OX=9606 GN=ORM2 PE=1 SV=2
44	1	Human_Uniprot_2018	sp|A0A075B6K5|LV39_HUMAN	278	12438	3	3	1	1	0.45	Immunoglobulin lambda variable 3-9 OS=Homo sapiens OX=9606 GN=IGLV3-9 PE=3 SV=1
45	1	Human_Uniprot_2018	sp|P08603|CFAH_HUMAN	278	143680	16	16	7	7	0.26	Complement factor H OS=Homo sapiens OX=9606 GN=CFH PE=1 SV=4
46	1	Human_Uniprot_2018	sp|P10909-2|CLUS_HUMAN	265	58537	14	14	8	8	0.9	Isoform 2 of Clusterin OS=Homo sapiens OX=9606 GN=CLU
47	1	Human_Uniprot_2018	sp|P01042-2|KNG1_HUMAN	264	48936	9	9	6	6	0.78	Isoform LMW of Kininogen-1 OS=Homo sapiens OX=9606 GN=KNG1
48	1	Human_Uniprot_2018	tr|B4E1Z4|B4E1Z4_HUMAN	235	143191	12	12	5	5	0.18	Myosin OS=Homo sapiens OX=9606 PE=1 SV=1
49	1	Human_Uniprot_2018	sp|P04264|K2C1_HUMAN	234	66170	9	9	6	6	0.53	Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6
50	1	Human_Uniprot_2018	tr|B0YIW2|B0YIW2_HUMAN	233	12864	5	5	2	2	1.05	Apolipoprotein C-III variant 1 OS=Homo sapiens OX=9606 GN=APOC3 PE=1 SV=1

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
51	1	Human_Uniprot_2018	sp|A0A0C4DH38|HV551_HUMAN	225	12837	8	8	3	3	1.94	Immunoglobulin heavy variable 5-51 OS=Homo sapiens OX=9606 GN=IGHV5-51 PE=3 SV=1
52	1	Human_Uniprot_2018	tr|A0A2R8Y7C0|A0A2R8Y7C0_HUMAN	222	13945	15	15	4	4	2.76	Hemoglobin subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1
53	1	Human_Uniprot_2018	sp|P27169|PON1_HUMAN	208	39877	7	7	5	5	0.8	Serum paraoxonase/arylesterase 1 OS=Homo sapiens OX=9606 GN=PON1 PE=1 SV=3
54	1	Human_Uniprot_2018	sp|P25311|ZA2G_HUMAN	193	34465	15	15	6	6	1.26	Zinc-alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=AZGP1 PE=1 SV=2
55	1	Human_Uniprot_2018	tr|C9JV77|C9JV77_HUMAN	174	40185	5	5	1	1	0.26	Alpha-2-HS-glycoprotein OS=Homo sapiens OX=9606 GN=AHSG PE=1 SV=1
56	1	Human_Uniprot_2018	sp|P07737|PROF1_HUMAN	163	15216	8	8	5	5	3.6	Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2
57	1	Human_Uniprot_2018	tr|S4R471|S4R471_HUMAN	155	21883	6	6	3	3	0.9	Protein AMBP (Fragment) OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1
58	1	Human_Uniprot_2018	sp|P02775|CXCL7_HUMAN	147	14171	6	6	2	2	0.92	Platelet basic protein OS=Homo sapiens OX=9606 GN=PPBP PE=1 SV=3
59	1	Human_Uniprot_2018	sp|P01597|KV139_HUMAN	145	12900	6	6	2	2	1.05	Immunoglobulin kappa variable 1-39 OS=Homo sapiens OX=9606 GN=IGKV1-39 PE=1 SV=2
60	1	Human_Uniprot_2018	sp|A0A0C4DH68|KV224_HUMAN	141	13185	4	4	2	2	1.01	Immunoglobulin kappa variable 2-24 OS=Homo sapiens OX=9606 GN=IGKV2-24 PE=3 SV=1
61	1	Human_Uniprot_2018	tr|V9GYE3|V9GYE3_HUMAN	140	5873	4	4	2	2	3.63	Apolipoprotein A-II OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1
62	1	Human_Uniprot_2018	sp|P12814-2|ACTN1_HUMAN	138	103215	8	8	5	5	0.26	Isoform 2 of Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1
63	1	Human_Uniprot_2018	sp|A0A075B6P5|KV228_HUMAN	131	13062	2	2	1	1	0.42	Immunoglobulin kappa variable 2-28 OS=Homo sapiens OX=9606 GN=IGKV2-28 PE=3 SV=1
64	1	Human_Uniprot_2018	sp|Q96PD5-2|PGRP2_HUMAN	130	68699	6	6	5	5	0.41	Isoform 2 of N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens OX=9606 GN=PGLYRP2
65	1	Human_Uniprot_2018	tr|F5H2D0|F5H2D0_HUMAN	125	78047	8	8	6	6	0.44	Clusterein OS=Homo sapiens OX=9606 GN=C1R PE=1 SV=3
66	1	Human_Uniprot_2018	sp|P02748|CO9_HUMAN	125	64615	5	5	3	3	0.24	Complement component C9 OS=Homo sapiens OX=9606 GN=C9 PE=1 SV=2
67	1	Human_Uniprot_2018	tr|A0A0J9YY99|A0A0J9YY99_HUMAN	121	13128	5	5	2	2	1.03	Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1
68	1	Human_Uniprot_2018	sp|P13645|K1C10_HUMAN	120	59020	4	4	4	4	0.37	Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6
69	1	Human_Uniprot_2018	sp|P36955|PEDF_HUMAN	119	46454	5	5	4	4	0.5	Pigment epithelium-derived factor OS=Homo sapiens OX=9606 GN=SERPINF1 PE=1 SV=4
70	1	Human_Uniprot_2018	sp|P02747|C1QC_HUMAN	116	25985	2	2	2	2	0.43	Osteonectin OS=Homo sapiens OX=9606 GN=C1QC PE=1 SV=3
71	1	Human_Uniprot_2018	tr|A0A087WWY3|A0A087WWY3_HUMAN	116	248149	9	9	8	8	0.16	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=1
72	1	Human_Uniprot_2018	tr|A0A2R8Y3M9|A0A2R8Y3M9_HUMAN	115	74186	4	4	2	2	0.14	Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1
73	1	Human_Uniprot_2018	tr|A0A0G2JPA8|A0A0G2JPA8_HUMAN	114	48135	5	5	3	3	0.34	Alpha-2-antiplasmin OS=Homo sapiens OX=9606 GN=SERPINF2 PE=1 SV=1
74	1	Human_Uniprot_2018	sp|P08185|CBG_HUMAN	113	45283	3	3	2	2	0.23	Von-willebrand factor OS=Homo sapiens OX=9606 GN=SERPINA6 PE=1 SV=1
75	1	Human_Uniprot_2018	sp|P02743|SAMP_HUMAN	109	25485	6	6	3	3	0.73	Serum amyloid P-component OS=Homo sapiens OX=9606 GN=APCS PE=1 SV=2
76	1	Human_Uniprot_2018	sp|A0A075B6S5|KV127_HUMAN	107	12874	3	3	1	1	0.43	Immunoglobulin kappa variable 1-27 OS=Homo sapiens OX=9606 GN=IGKV1-27 PE=3 SV=1
77	1	Human_Uniprot_2018	tr|X6RJP6|X6RJP6_HUMAN	107	21244	5	5	4	4	1.41	Transgelin-2 (Fragment) OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=1
78	1	Human_Uniprot_2018	sp|P05546|HEP2_HUMAN	106	57205	6	6	4	4	0.39	Heparin cofactor 2 OS=Homo sapiens OX=9606 GN=SERPIND1 PE=1 SV=3
79	1	Human_Uniprot_2018	sp|P01721|LV657_HUMAN	103	12729	2	2	1	1	0.44	Immunoglobulin lambda variable 6-57 OS=Homo sapiens OX=9606 GN=IGLV6-57 PE=1 SV=2
80	1	Human_Uniprot_2018	sp|P07996-2|TSP1_HUMAN	103	124062	3	3	2	2	0.08	Isoform 2 of Thrombospondin-1 OS=Homo sapiens OX=9606 GN=THBS1
81	1	Human_Uniprot_2018	sp|P01599|KV117_HUMAN	99	12941	4	4	2	2	1.04	Immunoglobulin kappa variable 1-17 OS=Homo sapiens OX=9606 GN=IGKV1-17 PE=1 SV=2
82	1	Human_Uniprot_2018	sp|P01031|CO5_HUMAN	94	189897	5	5	5	5	0.13	Thrombospondin OS=Homo sapiens OX=9606 GN=C5 PE=1 SV=4
83	1	Human_Uniprot_2018	sp|P43652|AFAM_HUMAN	93	70963	6	6	3	3	0.22	Afamin OS=Homo sapiens OX=9606 GN=AFM PE=1 SV=1
84	1	Human_Uniprot_2018	tr|A0A087X232|A0A087X232_HUMAN	91	77396	3	3	3	3	0.2	CXEL-7 OS=Homo sapiens OX=9606 GN=C1S PE=1 SV=1
85	1	Human_Uniprot_2018	sp|P01700|LV147_HUMAN	91	12447	2	2	1	1	0.45	Immunoglobulin lambda variable 1-47 OS=Homo sapiens OX=9606 GN=IGLV1-47 PE=1 SV=2
86	1	Human_Uniprot_2018	sp|P22792|CPN2_HUMAN	89	61373	5	5	3	3	0.26	Carboxypeptidase N subunit 2 OS=Homo sapiens OX=9606 GN=CPN2 PE=1 SV=3
87	1	Human_Uniprot_2018	tr|A0A0A0MSV6|A0A0A0MSV6_HUMAN	89	24243	3	3	2	2	0.47	Complement C1q subcomponent subunit B (Fragment) OS=Homo sapiens OX=9606 GN=C1QB PE=1 SV=6
88	1	Human_Uniprot_2018	tr|Q5VY30|Q5VY30_HUMAN	89	23301	4	4	2	2	0.49	Retinol-binding protein OS=Homo sapiens OX=9606 GN=RBP4 PE=1 SV=2
89	1	Human_Uniprot_2018	sp|P35579|MYH9_HUMAN	89	227646	7	7	7	7	0.16	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4
90	1	Human_Uniprot_2018	sp|A0A0C4DH31|HV118_HUMAN	88	12926	2	2	1	1	0.43	Immunoglobulin heavy variable 1-18 OS=Homo sapiens OX=9606 GN=IGHV1-18 PE=3 SV=1
91	1	Human_Uniprot_2018	sp|P18206-2|VINC_HUMAN	86	117220	7	7	4	4	0.17	Isoform 1 of Vinculin OS=Homo sapiens OX=9606 GN=VCL
92	1	Human_Uniprot_2018	tr|A0A024R0T9|A0A024R0T9_HUMAN	84	11277	2	2	1	1	0.5	Apolipoprotein C-II isoform 1 OS=Homo sapiens OX=9606 GN=APOC4-APOC2 PE=1 SV=1
93	1	Human_Uniprot_2018	tr|F5GZG1|F5GZG1_HUMAN	78	13937	3	3	1	1	0.39	Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=8
94	1	Human_Uniprot_2018	sp|A0A0B4J2D9|KVD13_HUMAN	78	12732	1	1	1	1	0.44	Immunoglobulin kappa variable 1D-13 OS=Homo sapiens OX=9606 GN=IGKV1D-13 PE=3 SV=1
95	1	Human_Uniprot_2018	sp|P06312|KV401_HUMAN	77	13486	4	4	2	2	0.99	Immunoglobulin kappa variable 4-1 OS=Homo sapiens OX=9606 GN=IGKV4-1 PE=1 SV=1
96	1	Human_Uniprot_2018	sp|P29622|KAIN_HUMAN	77	48682	2	2	2	2	0.21	Kallistatin OS=Homo sapiens OX=9606 GN=SERPINA4 PE=1 SV=3
97	1	Human_Uniprot_2018	sp|P35858-2|ALS_HUMAN	76	70990	5	5	4	4	0.3	Isoform 2 of Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens OX=9606 GN=IGFALS
98	1	Human_Uniprot_2018	tr|K7ERI9|K7ERI9_HUMAN	65	8642	4	4	2	2	1.88	Apolipoprotein C-I (Fragment) OS=Homo sapiens OX=9606 GN=APOC1 PE=1 SV=1
99	1	Human_Uniprot_2018	sp|Q9H4B7|TBB1_HUMAN	65	50865	2	2	2	2	0.2	Tubulin beta-1 chain OS=Homo sapiens OX=9606 GN=TUBB1 PE=1 SV=1
99	2	Human_Uniprot_2018	sp|A6NNZ2|TBB8L_HUMAN	42	50168	2	2	2	2	0.21	Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens OX=9606 PE=1 SV=1
100	1	Human_Uniprot_2018	tr|H0YAC1|H0YAC1_HUMAN	64	79001	4	4	3	3	0.2	Plasma kallikrein (Fragment) OS=Homo sapiens OX=9606 GN=KLKB1 PE=1 SV=1
101	1	Human_Uniprot_2018	sp|P00747|PLMN_HUMAN	63	93247	2	2	1	1	0.05	Plasminogen OS=Homo sapiens OX=9606 GN=PLG PE=1 SV=2
102	1	Human_Uniprot_2018	tr|E9PHK0|E9PHK0_HUMAN	62	18125	2	2	1	1	0.29	Tetranectin OS=Homo sapiens OX=9606 GN=CLEC3B PE=1 SV=1
103	1	Human_Uniprot_2018	sp|A0A0J9YX35|HV64D_HUMAN	60	12985	2	2	1	1	0.43	Immunoglobulin heavy variable 3-64D OS=Homo sapiens OX=9606 GN=IGHV3-64D PE=3 SV=1
104	1	Human_Uniprot_2018	sp|P04003|C4BPA_HUMAN	58	69042	3	3	2	2	0.15	C4b-binding protein alpha chain OS=Homo sapiens OX=9606 GN=C4BPA PE=1 SV=2
105	1	Human_Uniprot_2018	sp|P35908|K22E_HUMAN	55	65678	2	2	1	1	0.07	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
106	1	Human_Uniprot_2018	sp|Q86UX7-2|URP2_HUMAN	55	75953	2	2	2	2	0.13	Isoform 2 of Fermitin family homolog 3 OS=Homo sapiens OX=9606 GN=FERMT3
107	1	Human_Uniprot_2018	sp|P51884|LUM_HUMAN	54	38747	6	6	3	3	0.44	Lumican OS=Homo sapiens OX=9606 GN=LUM PE=1 SV=2
108	1	Human_Uniprot_2018	sp|P07360|CO8G_HUMAN	53	22435	4	4	3	3	0.87	Complement component C8 gamma chain OS=Homo sapiens OX=9606 GN=C8G PE=1 SV=3
109	1	Human_Uniprot_2018	sp|P00488|F13A_HUMAN	52	83728	1	1	1	1	0.06	Calpain OS=Homo sapiens OX=9606 GN=F13A1 PE=1 SV=4
110	1	Human_Uniprot_2018	sp|P02750|A2GL_HUMAN	47	38382	3	3	2	2	0.28	Leucine-rich alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=LRG1 PE=1 SV=2
111	1	Human_Uniprot_2018	tr|B0AZS6|B0AZS6_HUMAN	46	19174	2	2	1	1	0.27	cDNA, FLJ79516, highly similar to 14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1
112	1	Human_Uniprot_2018	sp|A0A0B4J1V0|HV315_HUMAN	46	13089	1	1	1	1	0.42	Immunoglobulin heavy variable 3-15 OS=Homo sapiens OX=9606 GN=IGHV3-15 PE=3 SV=1
113	1	Human_Uniprot_2018	sp|P80108|PHLD_HUMAN	44	92905	1	1	1	1	0.05	Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens OX=9606 GN=GPLD1 PE=1 SV=3
114	1	Human_Uniprot_2018	tr|G5E9F8|G5E9F8_HUMAN	44	61914	2	2	1	1	0.08	Protein S (Alpha), isoform CRA_b OS=Homo sapiens OX=9606 GN=PROS1 PE=1 SV=1
115	1	Human_Uniprot_2018	sp|A0A0A0MRZ8|KVD11_HUMAN	44	12731	1	1	1	1	0.44	Immunoglobulin kappa variable 3D-11 OS=Homo sapiens OX=9606 GN=IGKV3D-11 PE=3 SV=6
116	1	Human_Uniprot_2018	tr|A0A087X1J7|A0A087X1J7_HUMAN	43	25614	2	2	2	2	0.44	Glutathione peroxidase OS=Homo sapiens OX=9606 GN=GPX3 PE=1 SV=1
117	1	Human_Uniprot_2018	sp|P10643|CO7_HUMAN	42	96650	2	2	2	2	0.1	Complement component C7 OS=Homo sapiens OX=9606 GN=C7 PE=1 SV=2
118	1	Human_Uniprot_2018	sp|P08567|PLEK_HUMAN	41	40499	4	4	4	4	0.59	Pleckstrin OS=Homo sapiens OX=9606 GN=PLEK PE=1 SV=3
119	1	Human_Uniprot_2018	sp|P62328|TYB4_HUMAN	41	5050	1	1	1	1	1.45	Thymosin beta-4 OS=Homo sapiens OX=9606 GN=TMSB4X PE=1 SV=2
120	1	Human_Uniprot_2018	sp|A0A0B4J1Y9|HV372_HUMAN	41	13366	1	1	1	1	0.42	Immunoglobulin heavy variable 3-72 OS=Homo sapiens OX=9606 GN=IGHV3-72 PE=3 SV=1
121	1	Human_Uniprot_2018	sp|P18428|LBP_HUMAN	38	53521	1	1	1	1	0.09	Lipopolysaccharide-binding protein OS=Homo sapiens OX=9606 GN=LBP PE=1 SV=3
122	1	Human_Uniprot_2018	tr|K7EQQ3|K7EQQ3_HUMAN	38	39618	1	1	1	1	0.13	Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=1
123	1	Human_Uniprot_2018	sp|P00742|FA10_HUMAN	38	56065	2	2	2	2	0.18	Coagulation factor X OS=Homo sapiens OX=9606 GN=F10 PE=1 SV=2
124	1	Human_Uniprot_2018	sp|P04275|VWF_HUMAN	38	322401	1	1	1	1	0.01	von Willebrand factor OS=Homo sapiens OX=9606 GN=VWF PE=1 SV=4
125	1	Human_Uniprot_2018	tr|C9JF17|C9JF17_HUMAN	38	24541	3	3	2	2	0.46	Apolipoprotein D (Fragment) OS=Homo sapiens OX=9606 GN=APOD PE=1 SV=1
126	1	Human_Uniprot_2018	sp|P00748|FA12_HUMAN	37	70029	2	2	1	1	0.07	Coagulation factor XII OS=Homo sapiens OX=9606 GN=F12 PE=1 SV=3
127	1	Human_Uniprot_2018	tr|A0A075B7D0|A0A075B7D0_HUMAN	36	13117	1	1	1	1	0.42	Immunoglobulin heavy variable 1/OR15-1 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV1OR15-1 PE=1 SV=1
128	1	Human_Uniprot_2018	sp|P15814|IGLL1_HUMAN	36	23177	1	1	1	1	0.22	Immunoglobulin lambda-like polypeptide 1 OS=Homo sapiens OX=9606 GN=IGLL1 PE=1 SV=1
129	1	Human_Uniprot_2018	sp|Q9Y2I1-2|NISCH_HUMAN	36	111550	1	1	1	1	0.04	Isoform 2 of Nischarin OS=Homo sapiens OX=9606 GN=NISCH
130	1	Human_Uniprot_2018	tr|A0A096LPE2|A0A096LPE2_HUMAN	35	23510	2	2	1	1	0.22	SAA2-SAA4 readthrough OS=Homo sapiens OX=9606 GN=SAA2-SAA4 PE=4 SV=1
131	1	Human_Uniprot_2018	tr|A0A075B6Z2|A0A075B6Z2_HUMAN	34	2220	1	1	1	1	5.73	T cell receptor alpha joining 56 (Fragment) OS=Homo sapiens OX=9606 GN=TRAJ56 PE=4 SV=1
132	1	Human_Uniprot_2018	tr|Q5H928|Q5H928_HUMAN	34	17498	2	2	1	1	0.3	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=1
133	1	Human_Uniprot_2018	tr|A0A087WZB5|A0A087WZB5_HUMAN	34	33294	1	1	1	1	0.15	Beta-parvin OS=Homo sapiens OX=9606 GN=PARVB PE=1 SV=1
134	1	Human_Uniprot_2018	tr|H7C2U6|H7C2U6_HUMAN	34	25820	1	1	1	1	0.2	Protein NipSnap homolog 1 (Fragment) OS=Homo sapiens OX=9606 GN=NIPSNAP1 PE=1 SV=1
135	1	Human_Uniprot_2018	sp|P01602|KV105_HUMAN	32	12944	1	1	1	1	0.43	Immunoglobulin kappa variable 1-5 OS=Homo sapiens OX=9606 GN=IGKV1-5 PE=1 SV=2
136	1	Human_Uniprot_2018	tr|A0A2R8Y5J9|A0A2R8Y5J9_HUMAN	30	18097	1	1	1	1	0.29	Biotinidase, isoform CRA_c OS=Homo sapiens OX=9606 GN=BTD PE=1 SV=1
137	1	Human_Uniprot_2018	sp|A0A0C4DH33|HV124_HUMAN	30	12987	1	1	1	1	0.43	78-kd glucose dependent protein OS=Homo sapiens OX=9606 GN=IGHV1-24 PE=3 SV=1
138	1	Human_Uniprot_2018	sp|P05160|F13B_HUMAN	30	77742	1	1	1	1	0.06	Talin OS=Homo sapiens OX=9606 GN=F13B PE=1 SV=3
139	1	Human_Uniprot_2018	sp|A0A0A0MS15|HV349_HUMAN	29	13219	1	1	1	1	0.42	Integrin linked kinase OS=Homo sapiens OX=9606 GN=IGHV3-49 PE=3 SV=1
140	1	Human_Uniprot_2018	sp|P01742|HV169_HUMAN	29	12765	1	1	1	1	0.44	Immunoglobulin heavy variable 1-69 OS=Homo sapiens OX=9606 GN=IGHV1-69 PE=1 SV=2
141	1	Human_Uniprot_2018	sp|P13671|CO6_HUMAN	29	108367	1	1	1	1	0.04	Complement component C6 OS=Homo sapiens OX=9606 GN=C6 PE=1 SV=3
142	1	Human_Uniprot_2018	tr|F5GY80|F5GY80_HUMAN	28	61485	1	1	1	1	0.08	Complement component C8 beta chain OS=Homo sapiens OX=9606 GN=C8B PE=1 SV=1
143	1	Human_Uniprot_2018	sp|Q7Z7A1-5|CNTRL_HUMAN	28	269216	1	1	1	1	0.02	Isoform 5 of Centriolin OS=Homo sapiens OX=9606 GN=CNTRL
144	1	Human_Uniprot_2018	tr|A0A087WW43|A0A087WW43_HUMAN	27	75316	1	1	1	1	0.06	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens OX=9606 GN=ITIH3 PE=1 SV=1
145	1	Human_Uniprot_2018	tr|Q5T0R1|Q5T0R1_HUMAN	27	23972	1	1	1	1	0.22	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1
146	1	Human_Uniprot_2018	sp|P19438-5|TNR1A_HUMAN	25	25432	1	1	1	1	0.2	F-actin capping protein OS=Homo sapiens OX=9606 GN=TNFRSF1A
147	1	Human_Uniprot_2018	tr|K7EJY8|K7EJY8_HUMAN	25	16000	1	1	1	1	0.34	Galectin-3-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1
148	1	Human_Uniprot_2018	sp|Q2KHT3-2|CL16A_HUMAN	24	104222	1	1	1	1	0.05	Isoform 2 of Protein CLEC16A OS=Homo sapiens OX=9606 GN=CLEC16A
149	1	Human_Uniprot_2018	sp|Q6P1J6-3|PLB1_HUMAN	24	163492	1	1	1	1	0.03	Isoform 3 of Phospholipase B1, membrane-associated OS=Homo sapiens OX=9606 GN=PLB1
150	1	Human_Uniprot_2018	tr|A0A2R8Y5V9|A0A2R8Y5V9_HUMAN	24	28649	1	1	1	1	0.18	Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1
151	1	Human_Uniprot_2018	tr|H3BQ34|H3BQ34_HUMAN	24	30929	1	1	1	1	0.16	Pyruvate kinase OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1
152	1	Human_Uniprot_2018	tr|E7EUT5|E7EUT5_HUMAN	23	28024	1	1	1	1	0.18	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=1
153	1	Human_Uniprot_2018	tr|B1AHL2|B1AHL2_HUMAN	23	82439	1	1	1	1	0.06	Fibulin-1 OS=Homo sapiens OX=9606 GN=FBLN1 PE=1 SV=1
154	1	Human_Uniprot_2018	tr|A0A087WYX9|A0A087WYX9_HUMAN	22	107318	1	1	1	1	0.04	Collagen alpha-2(V) chain OS=Homo sapiens OX=9606 GN=COL5A2 PE=1 SV=1
155	1	Human_Uniprot_2018	sp|Q9H497-3|TOR3A_HUMAN	22	21338	1	1	1	1	0.24	Isoform 3 of Torsin-3A OS=Homo sapiens OX=9606 GN=TOR3A

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
156	1	Human_Uniprot_2018	sp|Q9BWW7|SCRT1_HUMAN	21	36175	1	1	1	1	0.14	Transcriptional repressor scratch 1 OS=Homo sapiens OX=9606 GN=SCRT1 PE=1 SV=1
157	1	Human_Uniprot_2018	tr|D6RAR4|D6RAR4_HUMAN	21	73660	1	1	1	1	0.07	ARP-2/3 OS=Homo sapiens OX=9606 GN=HGFAC PE=1 SV=1
158	1	Human_Uniprot_2018	sp|O14791-2|APOL1_HUMAN	21	46004	1	1	1	1	0.11	Isoform 2 of Apolipoprotein L1 OS=Homo sapiens OX=9606 GN=APOL1
159	1	Human_Uniprot_2018	tr|J3KPH2|J3KPH2_HUMAN	20	99298	1	1	1	1	0.05	Arachidonate lipoxygenase 3, isoform CRA_a OS=Homo sapiens OX=9606 GN=ALOXE3 PE=1 SV=1
160	1	Human_Uniprot_2018	sp|O75882-2|ATRN_HUMAN	19	146125	1	1	1	1	0.03	Isoform 2 of Attractin OS=Homo sapiens OX=9606 GN=ATRN
161	1	Human_Uniprot_2018	tr|J3QSE5|J3QSE5_HUMAN	19	29539	1	1	1	1	0.17	Phosphatidylcholine-sterol acyltransferase (Fragment) OS=Homo sapiens OX=9606 GN=LCAT PE=1 SV=1
162	1	Human_Uniprot_2018	sp|P01601|KVD16_HUMAN	18	12950	1	1	1	1	0.43	Immunoglobulin kappa variable 1D-16 OS=Homo sapiens OX=9606 GN=IGKV1D-16 PE=3 SV=2
163	1	Human_Uniprot_2018	tr|H0YCU9|H0YCU9_HUMAN	18	16833	1	1	1	1	0.32	Transgelin (Fragment) OS=Homo sapiens OX=9606 GN=TAGLN PE=1 SV=1
164	1	Human_Uniprot_2018	sp|P13224-2|GP1BB_HUMAN	18	44156	1	1	1	1	0.11	Isoform 2 of Platelet glycoprotein Ib beta chain OS=Homo sapiens OX=9606 GN=GP1BB
165	1	Human_Uniprot_2018	tr|U3KPZ0|U3KPZ0_HUMAN	18	12544	1	1	1	1	0.45	Triosephosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=1

	WITHOUT PAS - DAY 5 2(b)										
Family	**Member**	**Database**	**Accession**	**Score**	**Mass**	**Num. of matches**	**Num. of significant matches**	**Num. of sequences**	**Num. of significant sequences**	**emPAI**	**Description**
1	1	Human_Uniprot_2018	sp|P02768|ALBU_HUMAN	6494	71317	280	280	24	24	4.57	Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2
2	1	Human_Uniprot_2018	sp|P01024|CO3_HUMAN	4684	188569	175	175	48	48	2.41	Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2
3	1	Human_Uniprot_2018	sp|P04114|APOB_HUMAN	4531	516651	192	192	92	92	1.34	Apolipoprotein B-100 OS=Homo sapiens OX=9606 GN=APOB PE=1 SV=2
4	1	Human_Uniprot_2018	sp|P01023|A2MG_HUMAN	3005	164613	120	120	39	39	2.06	Alpha-2-macroglobulin OS=Homo sapiens OX=9606 GN=A2M PE=1 SV=3
5	1	Human_Uniprot_2018	sp|P02647|APOA1_HUMAN	2549	30759	105	105	23	23	37.62	Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1
6	1	Human_Uniprot_2018	sp|P01009|A1AT_HUMAN	2461	46878	88	88	17	17	4.5	Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3
6	2	Human_Uniprot_2018	tr|A0A024R6I7|A0A024R6I7_HUMAN	2368	46850	85	85	17	17	4.5	Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=1
7	1	Human_Uniprot_2018	tr|A0A0G2JL54|A0A0G2JL54_HUMAN	2353	189080	87	87	32	32	1.22	Complement C4-B OS=Homo sapiens OX=9606 GN=C4B_2 PE=1 SV=1
7	2	Human_Uniprot_2018	sp|P0C0L5|CO4B_HUMAN	2298	194170	84	84	32	32	1.18	Complement C4-B OS=Homo sapiens OX=9606 GN=C4B PE=1 SV=2
8	1	Human_Uniprot_2018	sp|P02787|TRFE_HUMAN	2174	79294	108	108	16	16	1.91	Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=3
9	1	Human_Uniprot_2018	tr|A0A0A0MS08|A0A0A0MS08_HUMAN	2079	44511	76	76	8	8	1.32	Immunoglobulin heavy constant gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1
9	2	Human_Uniprot_2018	sp|P01861|IGHG4_HUMAN	990	36431	31	31	6	6	1.17	Immunoglobulin heavy constant gamma 4 OS=Homo sapiens OX=9606 GN=IGHG4 PE=1 SV=1
9	3	Human_Uniprot_2018	sp|P01860|IGHG3_HUMAN	771	42287	38	38	5	5	0.74	Immunoglobulin heavy constant gamma 3 OS=Homo sapiens OX=9606 GN=IGHG3 PE=1 SV=2
9	4	Human_Uniprot_2018	sp|P01859|IGHG2_HUMAN	643	36505	38	38	4	4	0.9	Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=2
10	1	Human_Uniprot_2018	sp|P02675|FIBB_HUMAN	2059	56577	84	84	19	19	3.84	Fibrinogen beta chain OS=Homo sapiens OX=9606 GN=FGB PE=1 SV=2
11	1	Human_Uniprot_2018	sp|P02671-2|FIBA_HUMAN	2016	70227	81	81	15	15	1.92	Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA
12	1	Human_Uniprot_2018	sp|P01834|IGKC_HUMAN	1936	11929	76	76	6	6	9.3	Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2
13	1	Human_Uniprot_2018	sp|P02751-14|FINC_HUMAN	1287	252838	50	50	26	26	0.62	Isoform 14 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1
14	1	Human_Uniprot_2018	sp|P02766|TTHY_HUMAN	1102	15991	48	48	10	10	17.26	Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1
15	1	Human_Uniprot_2018	sp|P00450|CERU_HUMAN	1048	122983	46	46	17	17	0.92	Cyclophilin A =Homo sapiens OX=9606 GN=CP PE=1 SV=1
15	2	Human_Uniprot_2018	tr|E9PFZ2|E9PFZ2_HUMAN	758	109493	35	35	16	16	0.99	Ceruloplasmin OS=Homo sapiens OX=9606 GN=CP PE=1 SV=1
16	1	Human_Uniprot_2018	tr|B7ZKJ8|B7ZKJ8_HUMAN	974	104044	40	40	20	20	1.47	ITIH4 protein OS=Homo sapiens OX=9606 GN=ITIH4 PE=1 SV=1
17	1	Human_Uniprot_2018	tr|A0A1B0GUU9|A0A1B0GUU9_HUMAN	885	52518	34	34	8	8	1.05	Immunoglobulin heavy constant mu (Fragment) OS=Homo sapiens OX=9606 GN=IGHM PE=1 SV=1
18	1	Human_Uniprot_2018	tr|C9JC84|C9JC84_HUMAN	830	52932	36	36	9	9	1.43	Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=1
19	1	Human_Uniprot_2018	sp|A0M8Q6|IGLC7_HUMAN	739	11418	24	24	3	3	2.35	Immunoglobulin lambda constant 7 OS=Homo sapiens OX=9606 GN=IGLC7 PE=1 SV=3
19	2	Human_Uniprot_2018	sp|B9A064|IGLL5_HUMAN	637	23391	25	25	4	4	1.22	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens OX=9606 GN=IGLL5 PE=2 SV=2
20	1	Human_Uniprot_2018	sp|P01011|AACT_HUMAN	706	47792	20	20	10	10	1.67	Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=2
21	1	Human_Uniprot_2018	sp|P19827|ITIH1_HUMAN	687	101782	20	20	9	9	0.52	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens OX=9606 GN=ITIH1 PE=1 SV=3
22	1	Human_Uniprot_2018	tr|D6RF35|D6RF35_HUMAN	636	54583	27	27	6	6	0.68	Vitamin D-binding protein OS=Homo sapiens OX=9606 GN=GC PE=1 SV=1
23	1	Human_Uniprot_2018	tr|A0A2R8Y793|A0A2R8Y793_HUMAN	618	34405	25	25	9	9	2.41	Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1
23	2	Human_Uniprot_2018	sp|P68032|ACTC_HUMAN	323	42334	18	18	6	6	0.95	Actin, alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1
24	1	Human_Uniprot_2018	tr|A0A2R8Y7R2|A0A2R8Y7R2_HUMAN	529	12225	15	15	6	6	8.67	Pleckstrin OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=1
25	1	Human_Uniprot_2018	sp|P01019|ANGT_HUMAN	520	53406	16	16	7	7	0.85	Angiotensinogen OS=Homo sapiens OX=9606 GN=AGT PE=1 SV=1
26	1	Human_Uniprot_2018	sp|P01619|KV320_HUMAN	501	12663	8	8	2	2	1.08	Immunoglobulin kappa variable 3-20 OS=Homo sapiens OX=9606 GN=IGKV3-20 PE=1 SV=2
27	1	Human_Uniprot_2018	sp|P01008|ANT3_HUMAN	496	53025	23	23	10	10	1.42	Antithrombin-III OS=Homo sapiens OX=9606 GN=SERPINC1 PE=1 SV=1
28	1	Human_Uniprot_2018	tr|A0A0A0MS51|A0A0A0MS51_HUMAN	480	82759	15	15	7	7	0.49	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
29	1	Human_Uniprot_2018	sp|Q9Y490|TLN1_HUMAN	472	271766	24	24	20	20	0.42	Talin-1 OS=Homo sapiens OX=9606 GN=TLN1 PE=1 SV=3
30	1	Human_Uniprot_2018	tr|A0A286YEY1|A0A286YEY1_HUMAN	472	43620	14	14	3	3	0.38	Immunoglobulin heavy constant alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=1
30	2	Human_Uniprot_2018	sp|P01877|IGHA2_HUMAN	109	37366	5	5	3	3	0.46	Immunoglobulin heavy constant alpha 2 OS=Homo sapiens OX=9606 GN=IGHA2 PE=1 SV=4
31	1	Human_Uniprot_2018	sp|P06727|APOA4_HUMAN	453	45371	22	22	8	8	1.29	Apolipoprotein A-IV OS=Homo sapiens OX=9606 GN=APOA4 PE=1 SV=3
32	1	Human_Uniprot_2018	sp|P04196|HRG_HUMAN	451	60510	17	17	5	5	0.47	Histidine-rich glycoprotein OS=Homo sapiens OX=9606 GN=HRG PE=1 SV=1
33	1	Human_Uniprot_2018	tr|Q5T985|Q5T985_HUMAN	443	105606	20	20	9	9	0.49	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens OX=9606 GN=ITIH2 PE=1 SV=1
34	1	Human_Uniprot_2018	tr|A0A2Q2TTZ9|A0A2Q2TTZ9_HUMAN	441	11949	9	9	2	2	2.17	Immunoglobulin kappa variable 1-33 OS=Homo sapiens OX=9606 GN=IGKV1D-33 PE=1 SV=1
35	1	Human_Uniprot_2018	sp|P02649|APOE_HUMAN	424	36246	16	16	6	6	1.47	Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
36	1	Human_Uniprot_2018	sp|P05155-2|IC1_HUMAN	411	49954	18	18	7	7	0.93	Isoform 2 of Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1
37	1	Human_Uniprot_2018	sp|P04004|VTNC_HUMAN	370	55069	10	10	3	3	0.29	Vitronectin OS=Homo sapiens OX=9606 GN=VTN PE=1 SV=1
38	1	Human_Uniprot_2018	sp|P04217|A1BG_HUMAN	364	54790	25	25	9	9	1.16	Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=4
39	1	Human_Uniprot_2018	sp|P02790|HEMO_HUMAN	360	52385	21	21	7	7	0.87	Hemopexin OS=Homo sapiens OX=9606 GN=HPX PE=1 SV=2
40	1	Human_Uniprot_2018	tr|E9PIT3|E9PIT3_HUMAN	337	66792	14	14	4	4	0.33	Prothrombin OS=Homo sapiens OX=9606 GN=F2 PE=1 SV=1
41	1	Human_Uniprot_2018	tr|C9JEV0|C9JEV0_HUMAN	314	26508	9	9	4	4	1.02	Zinc-alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=AZGP1 PE=1 SV=1
42	1	Human_Uniprot_2018	sp|P02763|A1AG1_HUMAN	296	23725	17	17	5	5	1.67	Alpha-1-acid glycoprotein 1 OS=Homo sapiens OX=9606 GN=ORM1 PE=1 SV=1
42	2	Human_Uniprot_2018	sp|P19652|A1AG2_HUMAN	82	23873	8	8	3	3	0.8	Alpha-1-acid glycoprotein 2 OS=Homo sapiens OX=9606 GN=ORM2 PE=1 SV=2
43	1	Human_Uniprot_2018	sp|P10909-2|CLUS_HUMAN	286	58537	9	9	5	5	0.49	Isoform 2 of Clusterin OS=Homo sapiens OX=9606 GN=CLU
44	1	Human_Uniprot_2018	tr|J3QLC9|J3QLC9_HUMAN	282	41381	13	13	4	4	0.57	Haptoglobin (Fragment) OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1
44	2	Human_Uniprot_2018	sp|P00739-2|HPTR_HUMAN	233	44076	10	10	3	3	0.38	Isoform 2 of Haptoglobin-related protein OS=Homo sapiens OX=9606 GN=HPR
45	1	Human_Uniprot_2018	tr|A0A0G2JPA8|A0A0G2JPA8_HUMAN	272	48135	11	11	5	5	0.63	Alpha-2-antiplasmin OS=Homo sapiens OX=9606 GN=SERPINF2 PE=1 SV=1
46	1	Human_Uniprot_2018	tr|A0A0B4J2B5|A0A0B4J2B5_HUMAN	272	10764	7	7	2	2	1.35	Immunoglobulin heavy variable 3/OR16-9 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV3OR16-9 PE=1 SV=1
46	2	Human_Uniprot_2018	sp|P01780|HV307_HUMAN	115	13105	4	4	2	2	1.03	Caldesmon OS=Homo sapiens OX=9606 GN=IGHV3-7 PE=1 SV=2
47	1	Human_Uniprot_2018	tr|B0YIW2|B0YIW2_HUMAN	246	12864	7	7	3	3	1.94	Apolipoprotein C-III variant 1 OS=Homo sapiens OX=9606 GN=APOC3 PE=1 SV=1
48	1	Human_Uniprot_2018	sp|A0A075B6K5|LV39_HUMAN	234	12438	3	3	1	1	0.45	Immunoglobulin lambda variable 3-9 OS=Homo sapiens OX=9606 GN=IGLV3-9 PE=3 SV=1
49	1	Human_Uniprot_2018	tr|C9JV77|C9JV77_HUMAN	226	40185	6	6	1	1	0.26	Alpha-2-HS-glycoprotein OS=Homo sapiens OX=9606 GN=AHSG PE=1 SV=1
50	1	Human_Uniprot_2018	tr|Q60FE5|Q60FE5_HUMAN	226	280790	10	10	9	9	0.16	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=1
51	1	Human_Uniprot_2018	sp|P35579|MYH9_HUMAN	223	227646	15	15	13	13	0.31	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4
52	1	Human_Uniprot_2018	tr|B4E1Z4|B4E1Z4_HUMAN	217	143191	12	12	4	4	0.14	Myosin OS=Homo sapiens OX=9606 PE=1 SV=1
53	1	Human_Uniprot_2018	sp|P08603|CFAH_HUMAN	216	143680	12	12	5	5	0.18	Complement factor H OS=Homo sapiens OX=9606 GN=CFH PE=1 SV=4
54	1	Human_Uniprot_2018	sp|P01042-2|KNG1_HUMAN	214	48936	8	8	5	5	0.62	Isoform LMW of Kininogen-1 OS=Homo sapiens OX=9606 GN=KNG1
55	1	Human_Uniprot_2018	sp|P02775|CXCL7_HUMAN	212	14171	7	7	2	2	0.92	Platelet basic protein OS=Homo sapiens OX=9606 GN=PPBP PE=1 SV=3
56	1	Human_Uniprot_2018	tr|V9GYE3|V9GYE3_HUMAN	210	5873	4	4	2	2	3.63	Apolipoprotein A-II OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1
57	1	Human_Uniprot_2018	sp|A0A0C4DH38|HV551_HUMAN	208	12837	7	7	3	3	1.94	Immunoglobulin heavy variable 5-51 OS=Homo sapiens OX=9606 GN=IGHV5-51 PE=3 SV=1
58	1	Human_Uniprot_2018	tr|F5H2D0|F5H2D0_HUMAN	194	78047	9	9	6	6	0.44	Clusterein OS=Homo sapiens OX=9606 GN=C1R PE=1 SV=3
59	1	Human_Uniprot_2018	tr|A0A2R8Y7C0|A0A2R8Y7C0_HUMAN	194	13945	13	13	4	4	2.76	Hemoglobin subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1
60	1	Human_Uniprot_2018	sp|P07737|PROF1_HUMAN	187	15216	7	7	4	4	2.39	Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2
61	1	Human_Uniprot_2018	sp|P27169|PON1_HUMAN	181	39877	8	8	5	5	0.8	Serum paraoxonase/arylesterase 1 OS=Homo sapiens OX=9606 GN=PON1 PE=1 SV=3
62	1	Human_Uniprot_2018	sp|P43652|AFAM_HUMAN	181	70963	11	11	4	4	0.3	Afamin OS=Homo sapiens OX=9606 GN=AFM PE=1 SV=1
63	1	Human_Uniprot_2018	tr|H9KV75|H9KV75_HUMAN	179	95279	7	7	5	5	0.28	Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1
64	1	Human_Uniprot_2018	sp|P02750|A2GL_HUMAN	169	38382	7	7	4	4	0.63	Leucine-rich alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=LRG1 PE=1 SV=2
65	1	Human_Uniprot_2018	sp|P35858-2|ALS_HUMAN	167	70990	11	11	5	5	0.39	Isoform 2 of Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens OX=9606 GN=IGFALS
66	1	Human_Uniprot_2018	tr|X6RJP6|X6RJP6_HUMAN	155	21244	4	4	3	3	0.93	Transgelin-2 (Fragment) OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=1
67	1	Human_Uniprot_2018	sp|P02747|C1QC_HUMAN	124	25985	2	2	2	2	0.43	Osteonectin OS=Homo sapiens OX=9606 GN=C1QC PE=1 SV=3
68	1	Human_Uniprot_2018	tr|F5GZG1|F5GZG1_HUMAN	123	13937	2	2	1	1	0.39	Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=8
69	1	Human_Uniprot_2018	sp|P02743|SAMP_HUMAN	122	25485	5	5	3	3	0.73	Serum amyloid P-component OS=Homo sapiens OX=9606 GN=APCS PE=1 SV=2
70	1	Human_Uniprot_2018	tr|E9PHK0|E9PHK0_HUMAN	119	18125	2	2	1	1	0.29	Tetranectin OS=Homo sapiens OX=9606 GN=CLEC3B PE=1 SV=1
71	1	Human_Uniprot_2018	tr|A0A0A0MSV6|A0A0A0MSV6_HUMAN	118	24243	5	5	3	3	0.78	Complement C1q subcomponent subunit B (Fragment) OS=Homo sapiens OX=9606 GN=C1QB PE=1 SV=6
72	1	Human_Uniprot_2018	sp|Q9H4B7|TBB1_HUMAN	114	50865	4	4	3	3	0.32	Tubulin beta-1 chain OS=Homo sapiens OX=9606 GN=TUBB1 PE=1 SV=1
72	2	Human_Uniprot_2018	sp|P07437|TBB5_HUMAN	58	50095	3	3	3	3	0.33	Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2
72	3	Human_Uniprot_2018	sp|P04350|TBB4A_HUMAN	55	50010	3	3	3	3	0.33	Tubulin beta-4A chain OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=2
73	1	Human_Uniprot_2018	tr|S4R471|S4R471_HUMAN	114	21883	3	3	2	2	0.53	Protein AMBP (Fragment) OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1
74	1	Human_Uniprot_2018	sp|P51884|LUM_HUMAN	113	38747	9	9	3	3	0.44	Lumican OS=Homo sapiens OX=9606 GN=LUM PE=1 SV=2
75	1	Human_Uniprot_2018	tr|A0A0J9YY99|A0A0J9YY99_HUMAN	111	13128	6	6	2	2	1.03	Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1
76	1	Human_Uniprot_2018	tr|A0A2R8Y3M9|A0A2R8Y3M9_HUMAN	110	74186	3	3	2	2	0.14	Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1
77	1	Human_Uniprot_2018	sp|A0A0C4DH72|KV106_HUMAN	109	12860	4	4	1	1	0.43	Immunoglobulin kappa variable 1-6 OS=Homo sapiens OX=9606 GN=IGKV1-6 PE=3 SV=1

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
78	1	Human_Uniprot_2018	tr|A0A024R0T9|A0A024R0T9_HUMAN	109	11277	2	2	1	1	0.5	Apolipoprotein C-II isoform 1 OS=Homo sapiens OX=9606 GN=APOC4-APOC2 PE=1 SV=1
79	1	Human_Uniprot_2018	sp|P04264|K2C1_HUMAN	105	66170	3	3	2	2	0.15	Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6
80	1	Human_Uniprot_2018	sp|P01599|KV117_HUMAN	104	12941	4	4	2	2	1.04	Immunoglobulin kappa variable 1-17 OS=Homo sapiens OX=9606 GN=IGKV1-17 PE=1 SV=2
81	1	Human_Uniprot_2018	sp|P01031|CO5_HUMAN	102	189897	6	6	5	5	0.13	Complement C5 OS=Homo sapiens OX=9606 GN=C5 PE=1 SV=4
82	1	Human_Uniprot_2018	sp|P05546|HEP2_HUMAN	101	57205	8	8	4	4	0.39	Heparin cofactor 2 OS=Homo sapiens OX=9606 GN=SERPIND1 PE=1 SV=3
83	1	Human_Uniprot_2018	sp|P02748|CO9_HUMAN	100	64615	3	3	2	2	0.16	Complement component C9 OS=Homo sapiens OX=9606 GN=C9 PE=1 SV=2
84	1	Human_Uniprot_2018	sp|P01700|LV147_HUMAN	99	12447	2	2	1	1	0.45	Immunoglobulin lambda variable 1-47 OS=Homo sapiens OX=9606 GN=IGLV1-47 PE=1 SV=2
85	1	Human_Uniprot_2018	sp|P36955|PEDF_HUMAN	98	46454	6	6	5	5	0.66	Pigment epithelium-derived factor OS=Homo sapiens OX=9606 GN=SERPINF1 PE=1 SV=4
86	1	Human_Uniprot_2018	sp|A0A0C4DH68|KV224_HUMAN	97	13185	4	4	2	2	1.01	Immunoglobulin kappa variable 2-24 OS=Homo sapiens OX=9606 GN=IGKV2-24 PE=3 SV=1
87	1	Human_Uniprot_2018	tr|F5H1C6|F5H1C6_HUMAN	94	33292	2	2	2	2	0.32	Fermitin family homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=FERMT3 PE=1 SV=1
88	1	Human_Uniprot_2018	tr|Q5VY30|Q5VY30_HUMAN	92	23301	5	5	2	2	0.49	Retinol-binding protein OS=Homo sapiens OX=9606 GN=RBP4 PE=1 SV=2
89	1	Human_Uniprot_2018	sp|P18206-2|VINC_HUMAN	92	117220	4	4	3	3	0.13	Isoform 1 of Vinculin OS=Homo sapiens OX=9606 GN=VCL
90	1	Human_Uniprot_2018	sp|Q96PD5-2|PGRP2_HUMAN	85	68699	5	5	3	3	0.23	Isoform 2 of N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens OX=9606 GN=PGLYRP2
91	1	Human_Uniprot_2018	sp|A0A075B6S6|KVD30_HUMAN	82	13321	2	2	2	2	1	Immunoglobulin kappa variable 2D-30 OS=Homo sapiens OX=9606 GN=IGKV2D-30 PE=3 SV=1
92	1	Human_Uniprot_2018	sp|P29622|KAIN_HUMAN	77	48682	3	3	3	3	0.34	Kallistatin OS=Homo sapiens OX=9606 GN=SERPINA4 PE=1 SV=3
93	1	Human_Uniprot_2018	sp|A0A0C4DH31|HV118_HUMAN	74	12926	2	2	1	1	0.43	Immunoglobulin heavy variable 1-18 OS=Homo sapiens OX=9606 GN=IGHV1-18 PE=3 SV=1
94	1	Human_Uniprot_2018	sp|A0A0B4J2D9|KVD13_HUMAN	72	12732	1	1	1	1	0.44	Immunoglobulin kappa variable 1D-13 OS=Homo sapiens OX=9606 GN=IGKV1D-13 PE=3 SV=1
95	1	Human_Uniprot_2018	tr|A0A087X232|A0A087X232_HUMAN	66	77396	3	3	3	3	0.2	CXEL-7 subcomponent OS=Homo sapiens OX=9606 GN=C1S PE=1 SV=1
96	1	Human_Uniprot_2018	sp|P08185|CBG_HUMAN	64	45283	4	4	3	3	0.36	Von-willebrand factor OS=Homo sapiens OX=9606 GN=SERPINA6 PE=1 SV=1
97	1	Human_Uniprot_2018	sp|A0A075B6S5|KV127_HUMAN	64	12874	2	2	1	1	0.43	Immunoglobulin kappa variable 1-27 OS=Homo sapiens OX=9606 GN=IGKV1-27 PE=3 SV=1
98	1	Human_Uniprot_2018	sp|P07996|TSP1_HUMAN	62	133291	4	4	3	3	0.11	Thrombospondin-1 OS=Homo sapiens OX=9606 GN=THBS1 PE=1 SV=2
99	1	Human_Uniprot_2018	sp|P22792|CPN2_HUMAN	62	61373	5	5	3	3	0.26	Carboxypeptidase N subunit 2 OS=Homo sapiens OX=9606 GN=CPN2 PE=1 SV=3
100	1	Human_Uniprot_2018	sp|A0A0C4DH41|HV461_HUMAN	61	13172	2	2	1	1	0.42	Septin-2 OS=Homo sapiens OX=9606 GN=IGHV4-61 PE=3 SV=1
101	1	Human_Uniprot_2018	tr|A0A0A0MS09|A0A0A0MS09_HUMAN	56	47966	1	1	1	1	0.1	Immunoglobulin heavy constant delta (Fragment) OS=Homo sapiens OX=9606 GN=IGHD PE=1 SV=1
102	1	Human_Uniprot_2018	sp|P15814|IGLL1_HUMAN	55	23177	3	3	1	1	0.22	Immunoglobulin lambda-like polypeptide 1 OS=Homo sapiens OX=9606 GN=IGLL1 PE=1 SV=1
103	1	Human_Uniprot_2018	sp|P07360|CO8G_HUMAN	54	22435	3	3	3	3	0.87	Complement component C8 gamma chain OS=Homo sapiens OX=9606 GN=C8G PE=1 SV=3
104	1	Human_Uniprot_2018	tr|H0YAC1|H0YAC1_HUMAN	53	79001	2	2	2	2	0.13	Plasma kallikrein (Fragment) OS=Homo sapiens OX=9606 GN=KLKB1 PE=1 SV=1
105	1	Human_Uniprot_2018	sp|A0A0J9YX35|HV64D_HUMAN	53	12985	2	2	1	1	0.43	Immunoglobulin heavy variable 3-64D OS=Homo sapiens OX=9606 GN=IGHV3-64D PE=3 SV=1
106	1	Human_Uniprot_2018	sp|P62328|TYB4_HUMAN	49	5050	2	2	1	1	1.45	Thymosin beta-4 OS=Homo sapiens OX=9606 GN=TMSB4X PE=1 SV=2
107	1	Human_Uniprot_2018	sp|P00748|FA12_HUMAN	48	70029	2	2	1	1	0.07	Protein 14-3-3 =Homo sapiens OX=9606 GN=F12 PE=1 SV=3
108	1	Human_Uniprot_2018	sp|P00488|F13A_HUMAN	47	83728	2	2	2	2	0.12	Calpain OS=Homo sapiens OX=9606 GN=F13A1 PE=1 SV=4
109	1	Human_Uniprot_2018	sp|A0A0A0MS15|HV349_HUMAN	45	13219	2	2	1	1	0.42	Integrin linked kinase OS=Homo sapiens OX=9606 GN=IGHV3-49 PE=3 SV=1
110	1	Human_Uniprot_2018	tr|K7EJY8|K7EJY8_HUMAN	42	16000	1	1	1	1	0.34	Galectin-3-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1
111	1	Human_Uniprot_2018	sp|A0A0B4J1Y9|HV372_HUMAN	41	13366	1	1	1	1	0.42	Immunoglobulin heavy variable 3-72 OS=Homo sapiens OX=9606 GN=IGHV3-72 PE=3 SV=1
112	1	Human_Uniprot_2018	sp|P10643|CO7_HUMAN	41	96650	1	1	1	1	0.05	Complement component C7 OS=Homo sapiens OX=9606 GN=C7 PE=1 SV=2
113	1	Human_Uniprot_2018	tr|A0A087X1J7|A0A087X1J7_HUMAN	40	25614	2	2	2	2	0.44	Glutathione peroxidase OS=Homo sapiens OX=9606 GN=GPX3 PE=1 SV=1
114	1	Human_Uniprot_2018	sp|A0A0B4J1V0|HV315_HUMAN	40	13089	1	1	1	1	0.42	Immunoglobulin heavy variable 3-15 OS=Homo sapiens OX=9606 GN=IGHV3-15 PE=3 SV=1
115	1	Human_Uniprot_2018	tr|G3V1V0|G3V1V0_HUMAN	39	18311	1	1	1	1	0.29	Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1
116	1	Human_Uniprot_2018	tr|K7ERI9|K7ERI9_HUMAN	39	8642	3	3	2	2	1.88	Apolipoprotein C-I (Fragment) OS=Homo sapiens OX=9606 GN=APOC1 PE=1 SV=1

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
117	1	Human_Uniprot_2018	sp|P15169|CBPN_HUMAN	38	52538	2	2	2	2	0.2	Carboxypeptidase N catalytic chain OS=Homo sapiens OX=9606 GN=CPN1 PE=1 SV=1
118	1	Human_Uniprot_2018	tr|G5E9F8|G5E9F8_HUMAN	38	61914	2	2	2	2	0.16	Protein S (Alpha), isoform CRA_b OS=Homo sapiens OX=9606 GN=PROS1 PE=1 SV=1
119	1	Human_Uniprot_2018	tr|J3QRS3|J3QRS3_HUMAN	37	20501	1	1	1	1	0.25	Myosin regulatory light chain 12A OS=Homo sapiens OX=9606 GN=MYL12A PE=1 SV=1
120	1	Human_Uniprot_2018	tr|F5GY80|F5GY80_HUMAN	36	61485	2	2	2	2	0.17	Complement component C8 beta chain OS=Homo sapiens OX=9606 GN=C8B PE=1 SV=1
121	1	Human_Uniprot_2018	sp|P06312|KV401_HUMAN	35	13486	2	2	1	1	0.41	Immunoglobulin kappa variable 4-1 OS=Homo sapiens OX=9606 GN=IGKV4-1 PE=1 SV=1
122	1	Human_Uniprot_2018	sp|P13671|CO6_HUMAN	35	108367	1	1	1	1	0.04	Complement component C6 OS=Homo sapiens OX=9606 GN=C6 PE=1 SV=3
123	1	Human_Uniprot_2018	sp|P04003|C4BPA_HUMAN	34	69042	2	2	2	2	0.15	C4b-binding protein alpha chain OS=Homo sapiens OX=9606 GN=C4BPA PE=1 SV=2
124	1	Human_Uniprot_2018	tr|C9JF17|C9JF17_HUMAN	34	24541	1	1	1	1	0.21	Apolipoprotein D (Fragment) OS=Homo sapiens OX=9606 GN=APOD PE=1 SV=1
125	1	Human_Uniprot_2018	sp|P08567|PLEK_HUMAN	34	40499	1	1	1	1	0.12	Pleckstrin OS=Homo sapiens OX=9606 GN=PLEK PE=1 SV=3
126	1	Human_Uniprot_2018	tr|A0A1W2PQM2|A0A1W2PQM2_HUMAN	33	37312	1	1	1	1	0.13	Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1
127	1	Human_Uniprot_2018	tr|Q5H928|Q5H928_HUMAN	33	17498	2	2	1	1	0.3	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=1
128	1	Human_Uniprot_2018	sp|P0DJI8|SAA1_HUMAN	31	13581	2	2	2	2	0.98	Serum amyloid A-1 protein OS=Homo sapiens OX=9606 GN=SAA1 PE=1 SV=1
129	1	Human_Uniprot_2018	sp|O75882-2|ATRN_HUMAN	31	146125	2	2	2	2	0.07	Isoform 2 of Attractin OS=Homo sapiens OX=9606 GN=ATRN
130	1	Human_Uniprot_2018	sp|A0A0A0MRZ8|KVD11_HUMAN	29	12731	1	1	1	1	0.44	Immunoglobulin kappa variable 3D-11 OS=Homo sapiens OX=9606 GN=IGKV3D-11 PE=3 SV=6
131	1	Human_Uniprot_2018	sp|P00747|PLMN_HUMAN	28	93247	2	2	2	2	0.11	Plasminogen OS=Homo sapiens OX=9606 GN=PLG PE=1 SV=2
132	1	Human_Uniprot_2018	sp|P27105-2|STOM_HUMAN	26	13580	1	1	1	1	0.41	Calmodulin OS=Homo sapiens OX=9606 GN=STOM
133	1	Human_Uniprot_2018	sp|P18428|LBP_HUMAN	26	53521	1	1	1	1	0.09	Lipopolysaccharide-binding protein OS=Homo sapiens OX=9606 GN=LBP PE=1 SV=3
134	1	Human_Uniprot_2018	tr|G3V264|G3V264_HUMAN	25	19059	1	1	1	1	0.28	Plasma serine protease inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=SERPINA5 PE=1 SV=1
135	1	Human_Uniprot_2018	sp|P01602|KV105_HUMAN	25	12944	2	2	1	1	0.43	Immunoglobulin kappa variable 1-5 OS=Homo sapiens OX=9606 GN=IGKV1-5 PE=1 SV=2
136	1	Human_Uniprot_2018	tr|U3KPZ0|U3KPZ0_HUMAN	24	12544	1	1	1	1	0.45	Triosephosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=1
137	1	Human_Uniprot_2018	tr|A0A1B0GW50|A0A1B0GW50_HUMAN	24	137046	1	1	1	1	0.03	Zinc finger E-box-binding homeobox 2 OS=Homo sapiens OX=9606 GN=ZEB2 PE=1 SV=1
138	1	Human_Uniprot_2018	tr|Q5SRP5|Q5SRP5_HUMAN	24	14404	1	1	1	1	0.38	Apolipoprotein M OS=Homo sapiens OX=9606 GN=APOM PE=1 SV=1
139	1	Human_Uniprot_2018	tr|A0A0G2JIE7|A0A0G2JIE7_HUMAN	23	59607	1	1	1	1	0.08	Complement C2 OS=Homo sapiens OX=9606 GN=C2 PE=1 SV=1
140	1	Human_Uniprot_2018	tr|I3L1Z5|I3L1Z5_HUMAN	23	4999	1	1	1	1	1.45	Partner and localizer of BRCA2 (Fragment) OS=Homo sapiens OX=9606 GN=PALB2 PE=4 SV=1
141	1	Human_Uniprot_2018	tr|H0Y8L3|H0Y8L3_HUMAN	22	40108	1	1	1	1	0.12	Transforming growth factor-beta-induced protein ig-h3 (Fragment) OS=Homo sapiens OX=9606 GN=TGFBI PE=1 SV=1
142	1	Human_Uniprot_2018	sp|P05543|THBG_HUMAN	22	46637	1	1	1	1	0.11	Fibrinogen =Homo sapiens OX=9606 GN=SERPINA7 PE=1 SV=2
143	1	Human_Uniprot_2018	tr|D6RD66|D6RD66_HUMAN	22	27066	1	1	1	1	0.19	WD repeat-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=WDR1 PE=1 SV=1
144	1	Human_Uniprot_2018	sp|P01721|LV657_HUMAN	21	12729	1	1	1	1	0.44	Immunoglobulin lambda variable 6-57 OS=Homo sapiens OX=9606 GN=IGLV6-57 PE=1 SV=2
145	1	Human_Uniprot_2018	tr|A0A0C4DGN2|A0A0C4DGN2_HUMAN	21	28876	1	1	1	1	0.18	Sex hormone-binding globulin (Fragment) OS=Homo sapiens OX=9606 GN=SHBG PE=1 SV=1
146	1	Human_Uniprot_2018	tr|M0QX15|M0QX15_HUMAN	20	70245	1	1	1	1	0.07	Ankyrin repeat and LEM domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ANKLE1 PE=1 SV=3
147	1	Human_Uniprot_2018	tr|A0A2R8Y6G6|A0A2R8Y6G6_HUMAN	20	47696	1	1	1	1	0.1	Gelsolin OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1
148	1	Human_Uniprot_2018	sp|P04430|KV116_HUMAN	20	12838	1	1	1	1	0.43	Immunoglobulin kappa variable 1-16 OS=Homo sapiens OX=9606 GN=IGKV1-16 PE=1 SV=2
149	1	Human_Uniprot_2018	tr|A0A0A0MRJ7|A0A0A0MRJ7_HUMAN	20	253218	1	1	1	1	0.02	Coagulation factor V OS=Homo sapiens OX=9606 GN=F5 PE=1 SV=1
150	1	Human_Uniprot_2018	sp|P11021|BIP_HUMAN	20	72402	1	1	1	1	0.07	Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2
151	1	Human_Uniprot_2018	sp|P23083|HV102_HUMAN	20	13190	1	1	1	1	0.42	Immunoglobulin heavy variable 1-2 OS=Homo sapiens OX=9606 GN=IGHV1-2 PE=1 SV=2
152	1	Human_Uniprot_2018	tr|Q5T0R1|Q5T0R1_HUMAN	19	23972	1	1	1	1	0.22	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1

Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
153	1	Human_Uniprot_2018	tr|H0YIY1|H0YIY1_HUMAN	19	16645	1	1	1	1	0.32	X-linked retinitis pigmentosa GTPase regulator-interacting protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=RPGRIP1 PE=4 SV=1
154	1	Human_Uniprot_2018	sp|Q93045-2|STMN2_HUMAN	19	21902	1	1	1	1	0.24	Isoform 2 of Stathmin-2 OS=Homo sapiens OX=9606 GN=STMN2

WITHOUT PAS - DAY 7 3(b)										
Member	**Database**	**Accession**	**Score**	**Mass**	**Num. of matches**	**Num. of significant matches**	**Num. of sequences**	**Num. of significant sequences**	**emPAI**	**Description**
1	Human_Uniprot_2018	sp|P02768|ALBU_HUMAN	9447	71317	407	407	26	26	5.35	Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2
1	Human_Uniprot_2018	sp|P01024|CO3_HUMAN	4338	188569	170	170	48	48	2.41	Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2
1	Human_Uniprot_2018	sp|P04114|APOB_HUMAN	4183	516651	185	185	99	99	1.56	Apolipoprotein B-100 OS=Homo sapiens OX=9606 GN=APOB PE=1 SV=2
1	Human_Uniprot_2018	sp|P01023|A2MG_HUMAN	3747	164613	143	143	39	39	2.06	Alpha-2-macroglobulin OS=Homo sapiens OX=9606 GN=A2M PE=1 SV=3
1	Human_Uniprot_2018	sp|P02787|TRFE_HUMAN	3128	79294	126	126	19	19	2.92	Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=3
1	Human_Uniprot_2018	sp|P01009|A1AT_HUMAN	2762	46878	103	103	17	17	5.08	Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3
2	Human_Uniprot_2018	tr|A0A024R6I7|A0A024R6I7_HUMAN	2614	46850	99	99	17	17	5.08	Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=1
1	Human_Uniprot_2018	sp|P01834|IGKC_HUMAN	2645	11929	98	98	5	5	5.98	Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2
1	Human_Uniprot_2018	sp|P02647|APOA1_HUMAN	2226	30759	78	78	22	22	32.17	Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1
1	Human_Uniprot_2018	sp|P02675|FIBB_HUMAN	2210	56577	89	89	20	20	4.26	Fibrinogen beta chain OS=Homo sapiens OX=9606 GN=FGB PE=1 SV=2
1	Human_Uniprot_2018	sp|P0C0L5|CO4B_HUMAN	2179	194170	78	78	35	35	1.34	Complement C4-B OS=Homo sapiens OX=9606 GN=C4B PE=1 SV=2
2	Human_Uniprot_2018	tr|A0A0G2JL54|A0A0G2JL54_HUMAN	2168	189080	77	77	35	35	1.39	Complement C4-B OS=Homo sapiens OX=9606 GN=C4B_2 PE=1 SV=1
3	Human_Uniprot_2018	sp|P0C0L4|CO4A_HUMAN	1905	194261	73	73	34	34	1.28	Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=2
1	Human_Uniprot_2018	tr|A0A0A0MS08|A0A0A0MS08_HUMAN	2138	44511	85	85	8	8	1.32	Immunoglobulin heavy constant gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1
2	Human_Uniprot_2018	sp|P01861|IGHG4_HUMAN	1032	36431	32	32	5	5	0.9	Immunoglobulin heavy constant gamma 4 OS=Homo sapiens OX=9606 GN=IGHG4 PE=1 SV=1
3	Human_Uniprot_2018	sp|P01859|IGHG2_HUMAN	833	36505	47	47	5	5	1.16	Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=2
4	Human_Uniprot_2018	sp|P01860|IGHG3_HUMAN	813	42287	44	44	5	5	0.74	Immunoglobulin heavy constant gamma 3 OS=Homo sapiens OX=9606 GN=IGHG3 PE=1 SV=2
1	Human_Uniprot_2018	sp|P02671-2|FIBA_HUMAN	1551	70227	70	70	16	16	2.12	Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA
1	Human_Uniprot_2018	sp|P02766|TTHY_HUMAN	1246	15991	45	45	11	11	23.41	Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1
1	Human_Uniprot_2018	sp|P02751-10|FINC_HUMAN	1143	243068	47	47	23	23	0.56	Isoform 10 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1
1	Human_Uniprot_2018	sp|P00450|CERU_HUMAN	1008	122983	40	40	17	17	0.92	Cyclophilin A=Homo sapiens OX=9606 GN=CP PE=1 SV=1
2	Human_Uniprot_2018	tr|E9PFZ2|E9PFZ2_HUMAN	790	109493	35	35	16	16	0.99	Ceruloplasmin OS=Homo sapiens OX=9606 GN=CP PE=1 SV=1
1	Human_Uniprot_2018	tr|B7ZKJ8|B7ZKJ8_HUMAN	977	104044	39	39	21	21	1.59	ITIH4 protein OS=Homo sapiens OX=9606 GN=ITIH4 PE=1 SV=1
1	Human_Uniprot_2018	tr|C9JC84|C9JC84_HUMAN	949	52932	34	34	10	10	1.43	Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=1
1	Human_Uniprot_2018	sp|P19827|ITIH1_HUMAN	850	101782	26	26	10	10	0.59	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens OX=9606 GN=ITIH1 PE=1 SV=3
1	Human_Uniprot_2018	tr|A0A1B0GUU9|A0A1B0GUU9_HUMAN	801	52518	32	32	7	7	0.87	Immunoglobulin heavy constant mu (Fragment) OS=Homo sapiens OX=9606 GN=IGHM PE=1 SV=1
1	Human_Uniprot_2018	sp|P01619|KV320_HUMAN	780	12663	13	13	3	3	1.99	Immunoglobulin kappa variable 3-20 OS=Homo sapiens OX=9606 GN=IGKV3-20 PE=1 SV=2
1	Human_Uniprot_2018	sp|P01011|AACT_HUMAN	755	47792	20	20	11	11	1.94	Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=2
1	Human_Uniprot_2018	sp|A0M8Q6|IGLC7_HUMAN	722	11418	23	23	2	2	1.24	Immunoglobulin lambda constant 7 OS=Homo sapiens OX=9606 GN=IGLC7 PE=1 SV=3
2	Human_Uniprot_2018	sp|B9A064|IGLL5_HUMAN	578	23391	22	22	3	3	0.82	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens OX=9606 GN=IGLL5 PE=2 SV=2
1	Human_Uniprot_2018	sp|P01008|ANT3_HUMAN	655	53025	32	32	12	12	1.89	Antithrombin-III OS=Homo sapiens OX=9606 GN=SERPINC1 PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A286YEY1|A0A286YEY1_HUMAN	651	43620	18	18	3	3	0.38	Immunoglobulin heavy constant alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=1
2	Human_Uniprot_2018	tr|A0A0G2JMB2|A0A0G2JMB2_HUMAN	553	37283	16	16	3	3	0.46	Immunoglobulin heavy constant alpha 2 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA2 PE=1 SV=1
1	Human_Uniprot_2018	tr|Q5T985|Q5T985_HUMAN	599	105606	31	31	13	13	0.79	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens OX=9606 GN=ITIH2 PE=1 SV=1
1	Human_Uniprot_2018	tr|D6RF35|D6RF35_HUMAN	553	54583	23	23	8	8	0.99	Vitamin D-binding protein OS=Homo sapiens OX=9606 GN=GC PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A2R8Y793|A0A2R8Y793_HUMAN	540	34405	22	22	9	9	2.41	Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1
2	Human_Uniprot_2018	sp|P68032|ACTC_HUMAN	287	42334	10	10	5	5	0.74	Actin, alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1
1	Human_Uniprot_2018	sp|P04196|HRG_HUMAN	491	60510	20	20	6	6	0.59	Histidine-rich glycoprotein OS=Homo sapiens OX=9606 GN=HRG PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A2R8Y7R2|A0A2R8Y7R2_HUMAN	468	12225	13	13	5	5	5.63	Pleckstrin OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=1

Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
1	Human_Uniprot_2018	sp|P05155-2|IC1_HUMAN	441	49954	18	18	8	8	1.33	Isoform 2 of Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1
1	Human_Uniprot_2018	sp|P06727|APOA4_HUMAN	433	45371	21	21	8	8	1.29	Apolipoprotein A-IV OS=Homo sapiens OX=9606 GN=APOA4 PE=1 SV=3
1	Human_Uniprot_2018	sp|P02763|A1AG1_HUMAN	402	23725	20	20	6	6	2.25	Alpha-1-acid glycoprotein 1 OS=Homo sapiens OX=9606 GN=ORM1 PE=1 SV=1
2	Human_Uniprot_2018	sp|P19652|A1AG2_HUMAN	170	23873	11	11	3	3	0.8	Alpha-1-acid glycoprotein 2 OS=Homo sapiens OX=9606 GN=ORM2 PE=1 SV=2
1	Human_Uniprot_2018	tr|A0A2Q2TTZ9|A0A2Q2TTZ9_HUMAN	400	11949	8	8	2	2	2.17	Immunoglobulin kappa variable 1-33 OS=Homo sapiens OX=9606 GN=IGKV1D-33 PE=1 SV=1
1	Human_Uniprot_2018	sp|P02790|HEMO_HUMAN	397	52385	20	20	7	7	0.87	Hemopexin OS=Homo sapiens OX=9606 GN=HPX PE=1 SV=2
1	Human_Uniprot_2018	sp|P02649|APOE_HUMAN	392	36246	17	17	7	7	1.81	Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1
1	Human_Uniprot_2018	tr|E9PIT3|E9PIT3_HUMAN	370	66792	12	12	4	4	0.33	Prothrombin OS=Homo sapiens OX=9606 GN=F2 PE=1 SV=1
1	Human_Uniprot_2018	sp|Q9Y490|TLN1_HUMAN	360	271766	22	22	17	17	0.34	Talin-1 OS=Homo sapiens OX=9606 GN=TLN1 PE=1 SV=3
1	Human_Uniprot_2018	sp|P01019|ANGT_HUMAN	360	53406	12	12	5	5	0.55	Angiotensinogen OS=Homo sapiens OX=9606 GN=AGT PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A0A0MS51|A0A0A0MS51_HUMAN	350	82759	14	14	8	8	0.58	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
1	Human_Uniprot_2018	sp|P27169|PON1_HUMAN	340	39877	10	10	5	5	0.8	Serum paraoxonase/arylesterase 1 OS=Homo sapiens OX=9606 GN=PON1 PE=1 SV=3
1	Human_Uniprot_2018	sp|P00739|HPTR_HUMAN	338	39518	13	13	4	4	0.81	RAP-1 OS=Homo sapiens OX=9606 GN=HPR PE=2 SV=2
2	Human_Uniprot_2018	sp|P00738|HPT_HUMAN	333	45861	17	17	6	6	0.85	Haptoglobin OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1
1	Human_Uniprot_2018	sp|P04004|VTNC_HUMAN	309	55069	12	12	4	4	0.41	Vitronectin OS=Homo sapiens OX=9606 GN=VTN PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A0G2JPA8|A0A0G2JPA8_HUMAN	293	48135	10	10	5	5	0.63	Alpha-2-antiplasmin OS=Homo sapiens OX=9606 GN=SERPINF2 PE=1 SV=1
1	Human_Uniprot_2018	sp|P04217|A1BG_HUMAN	290	54790	17	17	9	9	1.16	Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=4
1	Human_Uniprot_2018	sp|P01042-2|KNG1_HUMAN	290	48936	7	7	4	4	0.47	Isoform LMW of Kininogen-1 OS=Homo sapiens OX=9606 GN=KNG1
1	Human_Uniprot_2018	sp|A0A075B6K5|LV39_HUMAN	285	12438	3	3	1	1	0.45	Immunoglobulin lambda variable 3-9 OS=Homo sapiens OX=9606 GN=IGLV3-9 PE=3 SV=1
1	Human_Uniprot_2018	sp|P10909-2|CLUS_HUMAN	273	58537	9	9	5	5	0.49	Isoform 2 of Clusterin OS=Homo sapiens OX=9606 GN=CLU
1	Human_Uniprot_2018	sp|P25311|ZA2G_HUMAN	266	34465	10	10	5	5	0.98	Zinc-alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=AZGP1 PE=1 SV=2
1	Human_Uniprot_2018	sp|A0A0C4DH38|HV551_HUMAN	247	12837	7	7	3	3	1.94	Immunoglobulin heavy variable 5-51 OS=Homo sapiens OX=9606 GN=IGHV5-51 PE=3 SV=1
1	Human_Uniprot_2018	tr|B0YIW2|B0YIW2_HUMAN	244	12864	5	5	2	2	1.05	Apolipoprotein C-III variant 1 OS=Homo sapiens OX=9606 GN=APOC3 PE=1 SV=1
1	Human_Uniprot_2018	sp|P43652|AFAM_HUMAN	244	70963	12	12	6	6	0.49	Afamin OS=Homo sapiens OX=9606 GN=AFM PE=1 SV=1
1	Human_Uniprot_2018	tr|C9JV77|C9JV77_HUMAN	243	40185	6	6	1	1	0.26	Alpha-2-HS-glycoprotein OS=Homo sapiens OX=9606 GN=AHSG PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A0B4J2B5|A0A0B4J2B5_HUMAN	224	10764	11	11	2	2	1.35	Immunoglobulin heavy variable 3/OR16-9 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV3OR16-9 PE=1 SV=1
2	Human_Uniprot_2018	sp|P01780|HV307_HUMAN	81	13105	5	5	2	2	1.03	Caldesmon OS=Homo sapiens OX=9606 GN=IGHV3-7 PE=1 SV=2
1	Human_Uniprot_2018	sp|P01597|KV139_HUMAN	223	12900	7	7	2	2	1.05	Immunoglobulin kappa variable 1-39 OS=Homo sapiens OX=9606 GN=IGKV1-39 PE=1 SV=2
1	Human_Uniprot_2018	sp|P08603|CFAH_HUMAN	217	143680	13	13	5	5	0.18	Complement factor H OS=Homo sapiens OX=9606 GN=CFH PE=1 SV=4
1	Human_Uniprot_2018	sp|P35579|MYH9_HUMAN	215	227646	9	9	8	8	0.18	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4
1	Human_Uniprot_2018	tr|V9GYE3|V9GYE3_HUMAN	200	5873	6	6	2	2	3.63	Apolipoprotein A-II OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1
1	Human_Uniprot_2018	tr|B4E1Z4|B4E1Z4_HUMAN	194	143191	8	8	4	4	0.14	Myosin OS=Homo sapiens OX=9606 PE=1 SV=1
1	Human_Uniprot_2018	sp|P07737|PROF1_HUMAN	190	15216	8	8	5	5	3.6	Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2
1	Human_Uniprot_2018	sp|A0A075B6S5|KV127_HUMAN	178	12874	5	5	1	1	0.43	Immunoglobulin kappa variable 1-27 OS=Homo sapiens OX=9606 GN=IGKV1-27 PE=3 SV=1
1	Human_Uniprot_2018	tr|B4DPQ0|B4DPQ0_HUMAN	156	83376	8	8	5	5	0.33	cDNA FLJ54471, highly similar to Complement C1r subcomponent (EC 3.4.21.41) OS=Homo sapiens OX=9606 GN=C1R PE=1 SV=1
1	Human_Uniprot_2018	tr|Q60FE5|Q60FE5_HUMAN	155	280790	10	10	10	10	0.18	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A2R8Y7C0|A0A2R8Y7C0_HUMAN	152	13945	10	10	4	4	2.76	Hemoglobin subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1
1	Human_Uniprot_2018	sp|P02747|C1QC_HUMAN	150	25985	2	2	2	2	0.43	Osteonectin OS=Homo sapiens OX=9606 GN=C1QC PE=1 SV=3
1	Human_Uniprot_2018	sp|P02775|CXCL7_HUMAN	144	14171	8	8	3	3	1.66	Platelet basic protein OS=Homo sapiens OX=9606 GN=PPBP PE=1 SV=3
1	Human_Uniprot_2018	tr|A0A0J9YY99|A0A0J9YY99_HUMAN	138	13128	5	5	2	2	1.03	Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A024R0T9|A0A024R0T9_HUMAN	137	11277	5	5	3	3	2.39	Apolipoprotein C-II isoform 1 OS=Homo sapiens OX=9606 GN=APOC4-APOC2 PE=1 SV=1
1	Human_Uniprot_2018	sp|P01031|CO5_HUMAN	135	189897	8	8	7	7	0.19	Thrombospondin OS=Homo sapiens OX=9606 GN=C5 PE=1 SV=4

Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
1	Human_Uniprot_2018	sp|Q96PD5-2|PGRP2_HUMAN	132	68699	6	6	5	5	0.41	Isoform 2 of N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens OX=9606 GN=PGLYRP2
1	Human_Uniprot_2018	sp|P08185|CBG_HUMAN	130	45283	3	3	3	3	0.36	Von-willebrand factor OS=Homo sapiens OX=9606 GN=SERPINA6 PE=1 SV=1
1	Human_Uniprot_2018	tr|H9KV75|H9KV75_HUMAN	129	95279	8	8	6	6	0.35	Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1
1	Human_Uniprot_2018	sp|P01700|LV147_HUMAN	129	12447	2	2	1	1	0.45	Immunoglobulin lambda variable 1-47 OS=Homo sapiens OX=9606 GN=IGLV1-47 PE=1 SV=2
1	Human_Uniprot_2018	sp|P02748|CO9_HUMAN	126	64615	3	3	2	2	0.16	Complement component C9 OS=Homo sapiens OX=9606 GN=C9 PE=1 SV=2
1	Human_Uniprot_2018	sp|A0A0C4DH68|KV224_HUMAN	125	13185	4	4	2	2	1.01	Immunoglobulin kappa variable 2-24 OS=Homo sapiens OX=9606 GN=IGKV2-24 PE=3 SV=1
1	Human_Uniprot_2018	sp|P02743|SAMP_HUMAN	124	25485	6	6	3	3	0.73	Serum amyloid P-component OS=Homo sapiens OX=9606 GN=APCS PE=1 SV=2
1	Human_Uniprot_2018	tr|Q5VY30|Q5VY30_HUMAN	122	23301	5	5	2	2	0.49	Retinol-binding protein OS=Homo sapiens OX=9606 GN=RBP4 PE=1 SV=2
1	Human_Uniprot_2018	sp|P02750|A2GL_HUMAN	118	38382	9	9	5	5	0.84	Leucine-rich alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=LRG1 PE=1 SV=2
1	Human_Uniprot_2018	sp|P07996|TSP1_HUMAN	114	133291	6	6	4	4	0.15	Thrombospondin-1 OS=Homo sapiens OX=9606 GN=THBS1 PE=1 SV=2
1	Human_Uniprot_2018	sp|A0A0C4DH31|HV118_HUMAN	114	12926	2	2	1	1	0.43	Immunoglobulin heavy variable 1-18 OS=Homo sapiens OX=9606 GN=IGHV1-18 PE=3 SV=1
1	Human_Uniprot_2018	tr|A0A0A0MSV6|A0A0A0MSV6_HUMAN	113	24243	5	5	3	3	0.78	Complement C1q subcomponent subunit B (Fragment) OS=Homo sapiens OX=9606 GN=C1QB PE=1 SV=6
1	Human_Uniprot_2018	sp|Q9H4B7|TBB1_HUMAN	112	50865	6	6	3	3	0.32	Tubulin beta-1 chain OS=Homo sapiens OX=9606 GN=TUBB1 PE=1 SV=1
2	Human_Uniprot_2018	sp|P07437|TBB5_HUMAN	92	50095	5	5	4	4	0.46	Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2
1	Human_Uniprot_2018	tr|S4R471|S4R471_HUMAN	111	21883	3	3	3	3	0.9	Protein AMBP (Fragment) OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1
1	Human_Uniprot_2018	sp|P36955|PEDF_HUMAN	110	46454	6	6	4	4	0.5	Pigment epithelium-derived factor OS=Homo sapiens OX=9606 GN=SERPINF1 PE=1 SV=4
1	Human_Uniprot_2018	sp|P01599|KV117_HUMAN	97	12941	2	2	2	2	1.04	Immunoglobulin kappa variable 1-17 OS=Homo sapiens OX=9606 GN=IGKV1-17 PE=1 SV=2
1	Human_Uniprot_2018	sp|A0A075B6S6|KVD30_HUMAN	89	13321	2	2	2	2	1	Immunoglobulin kappa variable 2D-30 OS=Homo sapiens OX=9606 GN=IGKV2D-30 PE=3 SV=1
2	Human_Uniprot_2018	sp|A0A075B6P5|KV228_HUMAN	72	13062	2	2	2	2	1.03	Immunoglobulin kappa variable 2-28 OS=Homo sapiens OX=9606 GN=IGKV2-28 PE=3 SV=1
1	Human_Uniprot_2018	sp|P01742|HV169_HUMAN	86	12765	3	3	2	2	1.06	Immunoglobulin heavy variable 1-69 OS=Homo sapiens OX=9606 GN=IGHV1-69 PE=1 SV=2
1	Human_Uniprot_2018	sp|P51884|LUM_HUMAN	86	38747	5	5	3	3	0.44	Lumican OS=Homo sapiens OX=9606 GN=LUM PE=1 SV=2
1	Human_Uniprot_2018	sp|P05546|HEP2_HUMAN	84	57205	6	6	4	4	0.39	Heparin cofactor 2 OS=Homo sapiens OX=9606 GN=SERPIND1 PE=1 SV=3
1	Human_Uniprot_2018	sp|P18206-2|VINC_HUMAN	84	117220	4	4	3	3	0.13	Isoform 1 of Vinculin OS=Homo sapiens OX=9606 GN=VCL
1	Human_Uniprot_2018	sp|P04264|K2C1_HUMAN	83	66170	6	6	3	3	0.24	Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6
1	Human_Uniprot_2018	tr|A0A096LPE2|A0A096LPE2_HUMAN	77	23510	4	4	2	2	0.49	SAA2-SAA4 readthrough OS=Homo sapiens OX=9606 GN=SAA2-SAA4 PE=4 SV=1
1	Human_Uniprot_2018	sp|A0A0C4DH29|HV103_HUMAN	77	13113	1	1	1	1	0.42	Immunoglobulin heavy variable 1-3 OS=Homo sapiens OX=9606 GN=IGHV1-3 PE=3 SV=1
1	Human_Uniprot_2018	tr|E9PHK0|E9PHK0_HUMAN	69	18125	1	1	1	1	0.29	Tetranectin OS=Homo sapiens OX=9606 GN=CLEC3B PE=1 SV=1
1	Human_Uniprot_2018	tr|F5H1C6|F5H1C6_HUMAN	68	33292	2	2	2	2	0.32	Fermitin family homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=FERMT3 PE=1 SV=1
1	Human_Uniprot_2018	sp|P04003|C4BPA_HUMAN	66	69042	3	3	2	2	0.15	C4b-binding protein alpha chain OS=Homo sapiens OX=9606 GN=C4BPA PE=1 SV=2
1	Human_Uniprot_2018	sp|A0A0J9YX35|HV64D_HUMAN	66	12985	3	3	1	1	0.43	Immunoglobulin heavy variable 3-64D OS=Homo sapiens OX=9606 GN=IGHV3-64D PE=3 SV=1
1	Human_Uniprot_2018	tr|B0AZS6|B0AZS6_HUMAN	65	19174	2	2	1	1	0.27	cDNA, FLJ79516, highly similar to 14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1
1	Human_Uniprot_2018	tr|X6RJP6|X6RJP6_HUMAN	65	21244	3	3	2	2	0.55	Transgelin-2 (Fragment) OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=1
1	Human_Uniprot_2018	sp|P35858-2|ALS_HUMAN	65	70990	6	6	4	4	0.3	Isoform 2 of Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens OX=9606 GN=IGFALS
1	Human_Uniprot_2018	tr|K7ERI9|K7ERI9_HUMAN	64	8642	5	5	2	2	1.88	Apolipoprotein C-I (Fragment) OS=Homo sapiens OX=9606 GN=APOC1 PE=1 SV=1
1	Human_Uniprot_2018	sp|P43251-2|BTD_HUMAN	63	62383	2	2	2	2	0.16	Isoform 2 of Biotinidase OS=Homo sapiens OX=9606 GN=BTD
1	Human_Uniprot_2018	sp|A0A0A0MRZ8|KVD11_HUMAN	63	12731	3	3	1	1	0.44	Immunoglobulin kappa variable 3D-11 OS=Homo sapiens OX=9606 GN=IGKV3D-11 PE=3 SV=6

Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
1	Human_Uniprot_2018	sp|P08567|PLEK_HUMAN	63	40499	3	3	3	3	0.42	Pleckstrin OS=Homo sapiens OX=9606 GN=PLEK PE=1 SV=3
1	Human_Uniprot_2018	sp|A0A0B4J2D9|KVD13_HUMAN	62	12732	1	1	1	1	0.44	Immunoglobulin kappa variable 1D-13 OS=Homo sapiens OX=9606 GN=IGKV1D-13 PE=3 SV=1
1	Human_Uniprot_2018	tr|A0A2R8Y3M9|A0A2R8Y3M9_HUMAN	62	74186	3	3	2	2	0.14	Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1
1	Human_Uniprot_2018	sp|P00747|PLMN_HUMAN	61	93247	3	3	2	2	0.11	Plasminogen OS=Homo sapiens OX=9606 GN=PLG PE=1 SV=2
1	Human_Uniprot_2018	tr|A0A087X1J7|A0A087X1J7_HUMAN	59	25614	2	2	1	1	0.2	Glutathione peroxidase OS=Homo sapiens OX=9606 GN=GPX3 PE=1 SV=1
1	Human_Uniprot_2018	sp|P00488|F13A_HUMAN	58	83728	2	2	2	2	0.12	Calpain OS=Homo sapiens OX=9606 GN=F13A1 PE=1 SV=4
1	Human_Uniprot_2018	tr|H0YAC1|H0YAC1_HUMAN	57	79001	2	2	2	2	0.13	Plasma kallikrein (Fragment) OS=Homo sapiens OX=9606 GN=KLKB1 PE=1 SV=1
1	Human_Uniprot_2018	sp|A0A0C4DH41|HV461_HUMAN	56	13172	2	2	1	1	0.42	Septin-2 OS=Homo sapiens OX=9606 GN=IGHV4-61 PE=3 SV=1
1	Human_Uniprot_2018	sp|P06312|KV401_HUMAN	54	13486	3	3	1	1	0.41	Immunoglobulin kappa variable 4-1 OS=Homo sapiens OX=9606 GN=IGKV4-1 PE=1 SV=1
1	Human_Uniprot_2018	sp|P01624|KV315_HUMAN	54	12602	3	3	2	2	1.08	Immunoglobulin kappa variable 3-15 OS=Homo sapiens OX=9606 GN=IGKV3-15 PE=1 SV=2
1	Human_Uniprot_2018	sp|P22792|CPN2_HUMAN	54	61373	2	2	2	2	0.17	Carboxypeptidase N subunit 2 OS=Homo sapiens OX=9606 GN=CPN2 PE=1 SV=3
1	Human_Uniprot_2018	sp|P23083|HV102_HUMAN	52	13190	2	2	1	1	0.42	Immunoglobulin heavy variable 1-2 OS=Homo sapiens OX=9606 GN=IGHV1-2 PE=1 SV=2
1	Human_Uniprot_2018	sp|P13671|CO6_HUMAN	52	108367	3	3	2	2	0.09	Complement component C6 OS=Homo sapiens OX=9606 GN=C6 PE=1 SV=3
1	Human_Uniprot_2018	sp|A0A0B4J1V0|HV315_HUMAN	51	13089	1	1	1	1	0.42	Immunoglobulin heavy variable 3-15 OS=Homo sapiens OX=9606 GN=IGHV3-15 PE=3 SV=1
1	Human_Uniprot_2018	tr|C9JF17|C9JF17_HUMAN	51	24541	3	3	3	3	0.77	Apolipoprotein D (Fragment) OS=Homo sapiens OX=9606 GN=APOD PE=1 SV=1
1	Human_Uniprot_2018	sp|P15814|IGLL1_HUMAN	50	23177	2	2	1	1	0.22	Immunoglobulin lambda-like polypeptide 1 OS=Homo sapiens OX=9606 GN=IGLL1 PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A1W2PQM2|A0A1W2PQM2_HUMAN	47	37312	1	1	1	1	0.13	Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1
1	Human_Uniprot_2018	sp|Q16610-2|ECM1_HUMAN	45	47154	1	1	1	1	0.1	Isoform 2 of Extracellular matrix protein 1 OS=Homo sapiens OX=9606 GN=ECM1
1	Human_Uniprot_2018	tr|Q5H928|Q5H928_HUMAN	40	17498	3	3	1	1	0.3	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=1
1	Human_Uniprot_2018	sp|P05160|F13B_HUMAN	38	77742	1	1	1	1	0.06	**Talin OS=Homo sapiens OX=9606 GN=F13B PE=1 SV=3**
1	Human_Uniprot_2018	tr|A0A0C4DH36|A0A0C4DH36_HUMAN	38	12921	1	1	1	1	0.43	Immunoglobulin heavy variable 3-38 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGHV3-38 PE=1 SV=1
1	Human_Uniprot_2018	tr|G3XAJ6|G3XAJ6_HUMAN	38	59296	1	1	1	1	0.08	Raft-linking protein, isoform CRA_c OS=Homo sapiens OX=9606 GN=RFTN1 PE=1 SV=1
1	Human_Uniprot_2018	sp|P62328|TYB4_HUMAN	37	5050	1	1	1	1	1.45	Thymosin beta-4 OS=Homo sapiens OX=9606 GN=TMSB4X PE=1 SV=2
1	Human_Uniprot_2018	tr|D6RAR4|D6RAR4_HUMAN	36	73660	1	1	1	1	0.07	ARP-2/3 OS=Homo sapiens OX=9606 GN=HGFAC PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A2R8Y5V9|A0A2R8Y5V9_HUMAN	35	28649	1	1	1	1	0.18	Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1
1	Human_Uniprot_2018	tr|G5E9F8|G5E9F8_HUMAN	35	61914	2	2	2	2	0.16	Protein S (Alpha), isoform CRA_b OS=Homo sapiens OX=9606 GN=PROS1 PE=1 SV=1
1	Human_Uniprot_2018	sp|P00748|FA12_HUMAN	35	70029	1	1	1	1	0.07	Protein 14-3-3 =Homo sapiens OX=9606 GN=F12 PE=1 SV=3
1	Human_Uniprot_2018	tr|B4DYP1|B4DYP1_HUMAN	35	20749	2	2	1	1	0.25	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens OX=9606 GN=DDAH1 PE=1 SV=1
1	Human_Uniprot_2018	sp|Q9HCK5|AGO4_HUMAN	34	98175	1	1	1	1	0.05	Protein argonaute-4 OS=Homo sapiens OX=9606 GN=AGO4 PE=1 SV=2
1	Human_Uniprot_2018	sp|P07360|CO8G_HUMAN	34	22435	2	2	2	2	0.52	Complement component C8 gamma chain OS=Homo sapiens OX=9606 GN=C8G PE=1 SV=3
1	Human_Uniprot_2018	sp|A0A0C4DH33|HV124_HUMAN	34	12987	1	1	1	1	0.43	78-kd glucose dependent protein OS=Homo sapiens OX=9606 GN=IGHV1-24 PE=3 SV=1
1	Human_Uniprot_2018	sp|P01602|KV105_HUMAN	34	12944	1	1	1	1	0.43	Immunoglobulin kappa variable 1-5 OS=Homo sapiens OX=9606 GN=IGKV1-5 PE=1 SV=2
1	Human_Uniprot_2018	sp|A0A0A0MS15|HV349_HUMAN	33	13219	3	3	2	2	1.01	Integrin linked kinase OS=Homo sapiens OX=9606 GN=IGHV3-49 PE=3 SV=1
1	Human_Uniprot_2018	tr|A0A087X232|A0A087X232_HUMAN	33	77396	3	3	3	3	0.2	CXEL-7 OS=Homo sapiens OX=9606 GN=C1S PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A087WSY5|A0A087WSY5_HUMAN	32	44564	1	1	1	1	0.11	Carboxypeptidase B2 OS=Homo sapiens OX=9606 GN=CPB2 PE=1 SV=1

Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
1	Human_Uniprot_2018	tr|F5GZG1|F5GZG1_HUMAN	29	13937	1	1	1	1	0.39	Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=8
1	Human_Uniprot_2018	tr|A0A0A0MS09|A0A0A0MS09_HUMAN	28	47966	2	2	2	2	0.22	Immunoglobulin heavy constant delta (Fragment) OS=Homo sapiens OX=9606 GN=IGHD PE=1 SV=1
1	Human_Uniprot_2018	tr|F5GY80|F5GY80_HUMAN	28	61485	1	1	1	1	0.08	Complement component C8 beta chain OS=Homo sapiens OX=9606 GN=C8B PE=1 SV=1
1	Human_Uniprot_2018	tr|J3KRP0|J3KRP0_HUMAN	28	51994	1	1	1	1	0.09	Beta-Ala-His dipeptidase OS=Homo sapiens OX=9606 GN=CNDP1 PE=1 SV=2
1	Human_Uniprot_2018	sp|O14791-2|APOL1_HUMAN	27	46004	1	1	1	1	0.11	Isoform 2 of Apolipoprotein L1 OS=Homo sapiens OX=9606 GN=APOL1
1	Human_Uniprot_2018	tr|H7BXY6|H7BXY6_HUMAN	26	24529	1	1	1	1	0.21	Tetraspanin OS=Homo sapiens OX=9606 GN=TSPAN14 PE=1 SV=1
1	Human_Uniprot_2018	tr|G3V264|G3V264_HUMAN	25	19059	1	1	1	1	0.28	Plasma serine protease inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=SERPINA5 PE=1 SV=1
1	Human_Uniprot_2018	sp|O75882-2|ATRN_HUMAN	25	146125	1	1	1	1	0.03	Isoform 2 of Attractin OS=Homo sapiens OX=9606 GN=ATRN
1	Human_Uniprot_2018	sp|P27105-2|STOM_HUMAN	25	13580	1	1	1	1	0.41	Calmodulin OS=Homo sapiens OX=9606 GN=STOM
1	Human_Uniprot_2018	tr|E9PI65|E9PI65_HUMAN	25	17962	1	1	1	1	0.3	Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1
1	Human_Uniprot_2018	tr|H3BM21|H3BM21_HUMAN	24	90173	1	1	1	1	0.05	Integrin beta (Fragment) OS=Homo sapiens OX=9606 PE=3 SV=1
1	Human_Uniprot_2018	sp|P10643|CO7_HUMAN	24	96650	1	1	1	1	0.05	Complement component C7 OS=Homo sapiens OX=9606 GN=C7 PE=1 SV=2
1	Human_Uniprot_2018	sp|Q86XN8-2|MEX3D_HUMAN	24	66995	1	1	1	1	0.07	Isoform 2 of RNA-binding protein MEX3D OS=Homo sapiens OX=9606 GN=MEX3D
1	Human_Uniprot_2018	sp|Q9UJT2|TSKS_HUMAN	24	65751	2	2	1	1	0.07	Testis-specific serine kinase substrate OS=Homo sapiens OX=9606 GN=TSKS PE=1 SV=3
1	Human_Uniprot_2018	tr|E5RIZ5|E5RIZ5_HUMAN	24	6288	1	1	1	1	1.04	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PPIA PE=1 SV=1
1	Human_Uniprot_2018	sp|P05543|THBG_HUMAN	24	46637	2	2	2	2	0.22	Fibrinogen OS=Homo sapiens OX=9606 GN=SERPINA7 PE=1 SV=2
1	Human_Uniprot_2018	tr|H7C0G1|H7C0G1_HUMAN	23	52912	1	1	1	1	0.09	Transmembrane protein 245 (Fragment) OS=Homo sapiens OX=9606 GN=TMEM245 PE=1 SV=1
1	Human_Uniprot_2018	tr|H0Y420|H0Y420_HUMAN	23	6739	1	1	1	1	0.95	Collagen alpha-1(XVII) chain (Fragment) OS=Homo sapiens OX=9606 GN=COL17A1 PE=4 SV=1
1	Human_Uniprot_2018	sp|P13645|K1C10_HUMAN	23	59020	1	1	1	1	0.08	Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6
1	Human_Uniprot_2018	sp|P19438-5|TNR1A_HUMAN	22	25432	1	1	1	1	0.2	F-actin capping protein OS=Homo sapiens OX=9606 GN=TNFRSF1A
1	Human_Uniprot_2018	tr|H3BMQ8|H3BMQ8_HUMAN	22	15624	1	1	1	1	0.35	Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=1
1	Human_Uniprot_2018	sp|O00322-2|UPK1A_HUMAN	21	30513	1	1	1	1	0.17	Isoform 2 of Uroplakin-1a OS=Homo sapiens OX=9606 GN=UPK1A
1	Human_Uniprot_2018	tr|J3QSE5|J3QSE5_HUMAN	21	29539	1	1	1	1	0.17	Phosphatidylcholine-sterol acyltransferase (Fragment) OS=Homo sapiens OX=9606 GN=LCAT PE=1 SV=1
1	Human_Uniprot_2018	tr|Q5T0R1|Q5T0R1_HUMAN	21	23972	1	1	1	1	0.22	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1
1	Human_Uniprot_2018	tr|G3V2D1|G3V2D1_HUMAN	20	24454	1	1	1	1	0.21	Ribosomal protein S6 kinase alpha-5 OS=Homo sapiens OX=9606 GN=RPS6KA5 PE=1 SV=1
1	Human_Uniprot_2018	sp|Q7Z7A1-5|CNTRL_HUMAN	20	269216	1	1	1	1	0.02	Isoform 5 of Centriolin OS=Homo sapiens OX=9606 GN=CNTRL
1	Human_Uniprot_2018	sp|Q9NQX4|MYO5C_HUMAN	20	203994	1	1	1	1	0.02	Unconventional myosin-Vc OS=Homo sapiens OX=9606 GN=MYO5C PE=1 SV=2
1	Human_Uniprot_2018	sp|Q9H497-3|TOR3A_HUMAN	20	21338	1	1	1	1	0.24	Isoform 3 of Torsin-3A OS=Homo sapiens OX=9606 GN=TOR3A
1	Human_Uniprot_2018	sp|Q92618|ZN516_HUMAN	19	126321	1	1	1	1	0.04	Zinc finger protein 516 OS=Homo sapiens OX=9606 GN=ZNF516 PE=1 SV=1
1	Human_Uniprot_2018	sp|O43318-2|M3K7_HUMAN	19	64930	1	1	1	1	0.08	Isoform 1A of Mitogen-activated protein kinase kinase kinase 7 OS=Homo sapiens OX=9606 GN=MAP3K7
1	Human_Uniprot_2018	tr|E7EUT5|E7EUT5_HUMAN	19	28024	1	1	1	1	0.18	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=1
1	Human_Uniprot_2018	tr|Q5SRP5|Q5SRP5_HUMAN	19	14404	1	1	1	1	0.38	Apolipoprotein M OS=Homo sapiens OX=9606 GN=APOM PE=1 SV=1
1	Human_Uniprot_2018	tr|J3KPH2|J3KPH2_HUMAN	18	99298	1	1	1	1	0.05	Arachidonate lipoxygenase 3, isoform CRA_a OS=Homo sapiens OX=9606 GN=ALOXE3 PE=1 SV=1
1	Human_Uniprot_2018	tr|K7EJY8|K7EJY8_HUMAN	18	16000	1	1	1	1	0.34	Galectin-3-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1
1	Human_Uniprot_2018	tr|A0A075B718|A0A075B718_HUMAN	18	18147	1	1	1	1	0.29	Spatacsin (Fragment) OS=Homo sapiens OX=9606 GN=SPG11 PE=1 SV=1
1	Human_Uniprot_2018	tr|H3BQD4|H3BQD4_HUMAN	17	12095	1	1	1	1	0.46	Ribosome biogenesis protein TSR3 homolog (Fragment) OS=Homo sapiens OX=9606 GN=TSR3 PE=4 SV=1
1	Human_Uniprot_2018	tr|K7EKP6|K7EKP6_HUMAN	17	13228	1	1	1	1	0.42	Cysteine protease ATG4D OS=Homo sapiens OX=9606 GN=ATG4D PE=4 SV=1

Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
1	Human_Uniprot_2018	tr|K7EJH2|K7EJH2_HUMAN	17	6390	1	1	1	1	1.02	Tripartite motif-containing protein 16 (Fragment) OS=Homo sapiens OX=9606 GN=TRIM16 PE=4 SV=1
1	Human_Uniprot_2018	tr|H7C0Y6|H7C0Y6_HUMAN	17	7315	1	1	1	1	0.86	Anillin (Fragment) OS=Homo sapiens OX=9606 GN=ANLN PE=1 SV=1
1	Human_Uniprot_2018	tr|H0YBK9|H0YBK9_HUMAN	17	19240	1	1	1	1	0.27	DENN domain-containing protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=DENND3 PE=1 SV=1
1	Human_Uniprot_2018	tr|H0Y9K7|H0Y9K7_HUMAN	16	26402	1	1	1	1	0.19	Splicing factor, proline- and glutamine-rich (Fragment) OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=1

Row_ID	Description	log 2 P1	log 2 P2	log 2 P3	log 2 WP1	log 2 WP2	log 2WP3	Average log 2 P1	Average log 2 WP 1	Count P	Count WP3	Fold Change	Sub cellular localization	P-value			
sp|A0A0C4DH38|HV551_HUMAN	Immunoglobulin kappa variable 2D-30 OS=Homo sapiens OX=9606 GN=IGKV2D-30 PE=3 SV=1	0.163498732		0.189033824	0.150559677	0.214124805	0.169925001	0.2	0.2	2	3	1.0	Cytoplasm	0.038			
sp|A0M8Q6|IGLC7_HUMAN	Caldesmon OS=Homo sapiens OX=9606 GN=IGHV3-7 PE=1 SV=2	0.613531653	-0.943416472	0.632268215	0.604071324	0.650764559	-1.234465254	0.1	0.0	3	3	0.1	Cytoplasm	0.672			
sp|B9A064|IGLL5_HUMAN	CXEL-7 OS=Homo sapiens OX=9606 GN=C1S PE=1 SV=1	-Infinity	-3.321928095	-1.251538767	-1.358453971	-1.184424571	-7.64385619	-2.3	-3.4	2	3	1.5	Extracellular	0.011			
sp|P00450|CERU_HUMAN	Kallistatin OS=Homo sapiens OX=9606 GN=SERPINA4 PE=1 SV=3	-1.59946207		-3.058893689	-5.64385619	-2.836501268	-3.251538767	-2.3	-3.9	2	3	1.7	Cytoplasm	0.012			
sp|P01008|ANT3_HUMAN	Actinin OS=Homo sapiens OX=9606 GN=C1QC PE=1 SV=3	0.422233001		0.443606651	-0.286304185	-0.64385619	0.10433666	0.4	-0.3	2	3	-0.6	Cytoskeleton	0.022			
sp|P01009|A1AT_HUMAN	Von-wille brand factor OS=Homo sapiens OX=9606 GN=SERPINA6 PE=1 SV=1	2.09085343	1.475084883	2.097610797	1.650764559	1.895302621	2.092545742	1.9	1.9	3	3	1.0	Endoplasmatic reticulum	0.336			
sp|P01011|AACT_HUMAN	Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=4	0.163498732	-0.514573173	0.189033824	-0.251538767	-0.168122759	0.169925001	-0.1	-0.1	3	3	1.5	Plasma membrane	0.456			
sp|P01023|A2MG_HUMAN	Immunoglobulin heavy constant alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=1	-0.029146346	-0.810966176	0.22650853	0.189033824	0.35614381	0.316145742	-0.2	0.3	3	3	-1.4	Cytoskeleton	0.412			
sp|P01024|CO3_HUMAN	Osteonectin OS=Homo sapiens OX=9606 GN=C1QC PE=1 SV=3	0.333423734	-0.104697379	0.604071324	0.659924558	0.704871964	0.673556424	0.3	0.7	3	3	2.4	Cytoskeleton	0.337	**log 2**	**≥ 1.5**	**up regulated**
sp|P01597|KV139_HUMAN	Myosin (EC 3.4.21.47) OS=Homo sapiens OX=9606 PE=1 SV=1	-2.120294234		-2	-2.184424571		-2.089267338	-2.1	-2.1	2	2	1.0	Extracellular	0.528	**log 2**	**≤ -0.5**	**down regulated**
sp|P01599|KV117_HUMAN	F-Actin capping protein OS=Homo sapiens OX=9606 GN=TNFRSF1A	-2.184424571	-1.64385619	-2.058893689	-2.251538767	-1.943416472	-2.152003093	-2.0	-2.1	3	3	1.1	Cytoskeleton	0.456			
sp|P01619|KV320_HUMAN	Septin-2 OS=Homo sapiens OX=9606 GN=IGKV2-24 PE=3 SV=1	0.22650853	-1.473931188	0.250961574	-2	-1.736965594	0.232660757	-0.3	-1.2	3	3	3.5	Extracellular	0.696			
sp|P01834|IGKC_HUMAN	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1	3.084064265	2.3950628	3.087462841	3.08236197	3.09085343	2.368768349	2.9	2.8	3	3	1.0	Cytoplasm	0.840			
sp|P01859|IGHG2_HUMAN	Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=4	-1.556393349	-2.473931188		-3.836501268	-3.058893689	-1.535331733	-2.0	-2.8	2	3	1.4	Cytoskeleton	0.145			
sp|P01861|IGHG4_HUMAN	Complement C1s subcomponent OS=Homo sapiens OX=9606 GN=C1S PE=1 SV=1	-1.514573173	-2.473931188	-3.321928095	-1.556393349	-1.358453971	-3.556393349	-2.4	-2.2	3	3	0.9	Cell surface	0.320			
sp|P02647|APOA1_HUMAN	Vinculin OS=Homo sapiens OX=9606 GN=S100A9 PE=1 SV=1	5.431288654	4.269781238	4.502075956	4.736063628	5.203201156	4.970623614	4.7	5.0	3	3	1.0	Endoplasmatic reticulum	0.250			
sp|P02649|APOE_HUMAN	Phosphatidylcholine-sterol acyltransferase (Fragment) OS=Homo sapiens OX=9606 GN=LCAT PE=1 SV=1	-1.514573173	-1.152003093	-1.434402824	-0.64385619	-0.535331733	-0.007231569	-1.4	-0.4	3	3	0.3	Extracellular	0.150			
sp|P02671-2|FIBA_HUMAN	Isoform 2 of Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens OX=9606 GN=IGFALS	-1.286304185	-0.971430848	-0.104697379	0.59454855	0.189033824	0.384049807	-0.8	0.4	3	3	-0.5	Cytoplasm	0.690			
sp|P02675|FIBB_HUMAN	Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=1	1.59454855	1.250961574	1.604071324	1.778208576	1.613531653	1.784503983	1.5	1.7	3	3	1.2	Cytoplasm	0.253			
sp|P02763|A1AG1_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=1	-0.234465254	-0.074000581	-1.358453971		-0.168122759	0.521050737	-0.6	0.2	3	2	-0.3	Extracellular	0.459			
sp|P02766|TTHY_HUMAN	Calmodulin OS=Homo sapiens OX=9606 GN=STOM	4.039138394	4.047887329	4.040892431	4.038260575	4.042644337	4.497931652	4.0	4.2	3	3	1.0	Plasma membrane	0.011			
sp|P02768|ALBU_HUMAN	Thrombospondin OS=Homo sapiens OX=9606 GN=C5 PE=1 SV=4	2.310340121	1.659924558	2.053111336	1.454175893	1.922197848	2.181102551	2.0	1.9	3	3	0.9	Extracellular	0.016			
sp|P02775|CXCL7_HUMAN	Fermitin family homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=FERMT3 PE=1 SV=1	-3.321928095	-2.321928095	-0.217591435	-3.473931188	-2.836501268	-0.242976753	-2.0	-2.2	3	3	1.1	Cytoplasm	0.095			
sp|P02787|TRFE_HUMAN	Plasma serine protease inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=SERPINA5 PE=1 SV=1	0.344828497	0.028569152	0.367371066	0.722466024	0.176322773	1.073820233	0.2	0.7	3	3	2.7	Cytoplasm	0.102			
sp|P02790|HEMO_HUMAN	Pleckstrin=Homo sapiens OX=9606 GN=HBB PE=1 SV=2	-2.120294234	-2.736965594	-3.836501268	-1.286304185	-3.473931188	-4.184424571	-2.9	-3.0	3	3	1.0	Cytoskeleton	0.321			
sp|P04114|APOB_HUMAN	ARP-2/3 OS=Homo sapiens OX=9606 GN=HGFAC PE=1 SV=1	-1.836501268		-2.556393349	-1.321928095	-0.836501268	-0.424687669	-2.2	-0.9	2	3	0.4	Cytoplasm	0.141			
sp|P05155-2|IC1_HUMAN	Complement C5 OS=Homo sapiens OX=9606 GN=C5 PE=1 SV=4	-1.736965594		-2.943416472		-2.736965594	-0.957355663	-2.3	-1.8	2	2	0.8	Cytoskeleton	0.096			
sp|P06727|APOA4_HUMAN	Protein 14-3-3 OS=Homo sapiens OX=9606 GN=F12 PE=1 SV=3	-1.089267338	-0.810966176	-1.029146346	-0.49410907	-0.971430848	-1.074000581	-1.0	-0.8	3	3	0.9	Extracellular	0.018			
sp|P07737|PROF1_HUMAN	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=1	0.650764559	-0.358453971	0.669026766	1.469885976	0.687060688	1.477677328	0.3	1.2	3	3	3.8	Plasma membrane	0.145			
tr|A0A0A0MS08|A0A0A0MS08_HUMAN	Integrin linked kinase OS=Homo sapiens OX=9606 GN=IGHV3-49 PE=3 SV=1	-1.888968688	-0.736965594	-3.64385619	-1.029146346	-0.888968688	-0.985644707	-2.1	-1.0	3	3	0.5	Cytoplasm	0.532			
tr|A0A0B4J2B5|A0A0B4J2B5_HUMAN	Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=4	-0.915935735	-0.666576266	-0.862496476	0.831877241	-0.810966176	-0.902389203	-0.8	-0.3	3	3	0.4	Cytoskeleton	0.736			
tr|A0A0G2JL54|A0A0G2JL54_HUMAN	Calpain OS=Homo sapiens OX=9606 GN=F13A1 PE=1 SV=4	-1.514573173		-3.184424571	-1.556393349	-1.184424571	-0.798366139	-2.3	-1.2	2	3	0.5	Cytoplasm	0.130			
tr|A0A0J9YY99|A0A0J9YY99_HUMAN	Corticosteroid-binding globulin OS=Homo sapiens OX=9606 GN=SERPINA6 PE=1 SV=1	-2.251538767	-1.689659879	-2.120294234	-2.321928095	-2	-2.217591435	-2.0	-2.2	3	3	1.1	Cytoplasm	0.253			
tr|A0A1B0GUU9|A0A1B0GUU9_HUMAN	Immunoglobulin heavy constant alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=1	-2.120294234		-2	-2.184424571	-1.888968688	-4.184424571	-2.1	-2.8	2	3	1.3	Cytoplasm	0.445			
tr|A0A2Q2TTZ9|A0A2Q2TTZ9_HUMAN	78-KD glucose dependent protein OS=Homo sapiens OX=9606 GN=IGHV1-18 PE=3 SV=1	-1.556393349	-1.184424571	-1.473931188	-1.59946207	0.475084883	0.438292852	-1.4	-0.2	3	3	0.2	Cytoplasm	0.497			
tr|A0A2R8Y793|A0A2R8Y793_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2	0.201633861		0.22650853	0.189033824	0.704871964	0.673556424	0.2	0.5	2	3	2.4	Extracellular	0.653			
tr|A0A2R8Y7C0|A0A2R8Y7C0_HUMAN	RAP-1 OS=Homo sapiens OX=9606 GN=HPR PE=2 SV=2	-0.184424571	1.028569152	0.970853654	0.948600847	0.98550043	0.959770155	0.6	1.0	3	3	1.6	Cytoplasm	0.425			

Row_ID	Description	log 2 P1	log 2 P2	log 2 P3	log 2 WP1	log 2 WP2	log 2WP3	Average log 2 P1	Average log 2 WP 1	Count P	Count WP3	Fold Change	Sub cellular localization	P-value
tr|B0YIW2|B0YIW2_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=1	-2.120294234	0.286881148	-2	-2.184424571	0.214124805	-2.089267338	-1.3	-1.4	3	3	1.1	Cytoskeleton	0.029
tr|B7ZKJ8|B7ZKJ8_HUMAN	Isoform 2 of Apolipoprotein L1 OS=Homo sapiens OX=9606 GN=APOL1	-1.184424571	-2.556393349	-0.836501268	-2.120294234	-0.535331733	-0.367731785	-1.5	-1.0	3	3	0.7	Cytoplasm	0.121
tr|C9JC84|C9JC84_HUMAN	Fibrinogen OS=Homo sapiens OX=9606 GN=SERPINA7 PE=1 SV=2	-1.321928095	-1.689659879	0.137503524	-0.736965594	-0.621488377	-0.701341684	-1.0	-0.7	3	3	0.7	Extracellular	0.018
tr|E9PFZ2|E9PFZ2_HUMAN	Cyclophilin A=Homo sapiens OX=9606 GN=CP PE=1 SV=1	-1.152003093		-2.395928676		-2.251538767	-2.514573173	-1.8	-2.4	2	2	1.3	Plasma membrane	0.025
tr|K7ERI9|K7ERI9_HUMAN	Complement C5 OS=Homo sapiens OX=9606 GN=C5 PE=1 SV=4	0.084064265	0.214124805	0.111031312	0.070389328	0.137503524	0.09085343	0.1	0.1	3	3	0.7	Extracellular	0.109
tr|V9GYE3|V9GYE3_HUMAN	Clusterein=Homo sapiens OX=9606 GN=C1R PE=1 SV=3	1.49057013	1.541019153	1.500802053	1.485426827	1.510961919	1.493134922	1.5	1.5	3	3	1.0	Other cell body	0.852
sp|P01008|ANT3_HUMAN	Gelsolin OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1	0.422233001		0.443606651	-0.286304185	-0.64385619	0.10433666	0.4	-0.3	2	3	-0.6	Plasma membrane	0.125
sp|P01009|A1AT_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3	2.09085343	1.475084883	2.097610797	1.650764559	1.895302621	2.092545742	1.9	1.9	3	3	1.0	Cytoskeleton	0.324
sp|P01011|AACT_HUMAN	Isoform 2 of Integrin alpha-IIb OS=Homo sapiens OX=9606 GN=ITGA2B	0.163498732	-0.514573173	0.189033824	-0.251538767	-0.168122759	0.169925001	-0.1	-0.1	3	3	1.5	Extracellular	0.033
sp|P01019|ANGT_HUMAN	Interferon-induced very large GTPase 1 OS=Homo sapiens OX=9606 GN=GVINP1 PE=2 SV=2			-4.321928095	-5.64385619	-3.836501268		-4.3	-4.7	1	2	1.1	Cytoskeleton	0.121

Showing differential expression of proteins with fold change. Fold change >1.5 is considered as up-regulation of protein expression while fold change < -0.98 consider as down-regulationofproteinexpression as compared to control group. Student T test was caaried out to consider significantly

RECOMMENDATIONS

Recommendations

- Simple steps such as proper donor arm cleaning along with proper blood collection preparation and storage techniques along with proper emphasis on storage temperature regulation will help in maintenance of quality standards of PCs.
- Morphological parameters like, MPV, PDW provide an important simple, practical, effortless and cost effective tool, which can be suitable for use in daily practice to predict thrombocytopenia caused by acute febrile illness.
- Regular utilization of blood bags with separate sample collection pouches should be encouraged to reduce the risk of phlebotomy induced bacterial contamination of PCs. Current study highlight the fact that automated bacterial detection system along with regular pH estimation can be considered as an effective intervention to mitigate the risk associated with bacterial contamination of PCs in routine practice with excellent results. Standardization and promotion of routine QC measures such as, regular use of swirling tests and pH strips should be encouraged on a wider scale.
- The current study shows that ELISA as a diagnostic tool is scientifically prudent, technically feasible and economically viable alternative particularly in a resource constraint set up. Hence, efforts must be made to encourage standard methodologies such as ELISA to maintain the optimum QC of PCs.
- While our initial in-vitro data on the novel PAS is extremely promising, further in-vivo and eventually clinical studies are required to determine if the in-vitro benefits, as noted in current study can be translated in-vivo with improved clinical outcomes. In such a scenario PAS provides us the mechanism to extend the shelf life of PCs without compromising the quality parameters.
- CD62P (P-selectin) is a sensitive PC quality marker. Its expression measures platelet secretion and indicates the level of PC activation reflecting the quality of stored platelets during extended storage period.
- Evaluation of various PC activation markers on different sub populations can be an additional valid tool in QC of PCs, and could be a novel approach based on molecular diagnosis towards better platelet inventory management during extended period of storage as noted in our study.
- Platelet proteomic investigations have provided sufficient knowledge and permitted a more detailed understanding of PCs in relation to specific protein actions which can be developed into practical applications by regulating platelet protein synthesis pathways. Present study we have identified 34 such novel platelet proteins which can be analyzed further in future studies.
- Recently BC-PC has been considered as a blood component as per the Drugs and Cosmetic (Second Amendment) Rules, 2020, Government of India for routine clinical use. The findings and information generated from this study can provide vital inputs and scientific evidence to promote the use of this product for improving the quality of patient care and management.